

SEQUENCE LISTING

<110> Zoghbi, Huda
Ben-Arie, Nissim
Bellen, Hugo
Bermingham, Nessim
Hassan, Bassem

<120> COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN ATONAL-
ASSOCIATED SEQUENCE FOR DEAFNESS, OSTEOARTHRITIS, AND ABNORMAL CELL
PROLIFERATION

<130> HO-P01899US3/09906355/OTA 99-47

<140> US 09/980,381

<141> 2001-11-30

<150> US 60/137,060

<151> 1999-06-01

<150> US 60/176,993

<151> 2000-01-19

<150> PCT/US00/15410

<151> 2000-06-01

<160> 69

<170> PatentIn version 3.0

<210> 1

<211> 1065

<212> DNA

<213> HUMAN

<400> 1

```
atgtcccgcc tgctgcatgc agaagagtgg gctgaagtga aggagttggg agaccaccat      60
cgccagcccc agccgcatca tctcccgcaa ccgccgccgc cgccgcagcc acctgcaact      120
ttgcaggcga gagagcatcc cgtctacccg cctgagctgt ccctcctgga cagcaccgac      180
ccacgcgcct ggctggctcc cactttgcag ggcatctgca cggcacgcgc cgcccagtat      240
ttgctacatt ccccgagct ggggtgctca gaggccgctg cgccccggga cgaggtggac      300
ggccgggggg agctggtaag gaggagcagc ggcggtgcca gcagcagcaa gagccccggg      360
ccggtgaaag tgcgggaaca gctgtgcaag ctgaaaggcg ggggtgtggt agacgagctg      420
ggctgcagcc gccaacgggc cccttcagc aaacaggtga atggggtgca gaagcagaga      480
cggctagcag ccaacgccag ggagcggcgc aggatgcatg ggctgaacca cgcttcgac      540
cagctgcgca atgttatccc gtcgttcaac aacgacaaga agctgtccaa atatgagacc      600
ctgcagatgg cccaaatcta catcaacgcc ttgtccgagc tgctacaaac gccagcgga      660
ggggaacagc caccgccgcc tccagcctcc tgcaaaagcg accaccacca ccttcgcacc      720
gcggcctcct atgaaggggg cgcgggcaac gcgaccgcag ctggggctca gcaggttcc      780
```

09980381-030603

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
 225 230 235 240
 Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
 245 250 255
 Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
 260 265 270
 Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
 275 280 285
 Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
 290 295 300
 Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
 305 310 315 320
 Gln Pro Val Gln Glu Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg
 325 330 335
 Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu
 340 345 350

Ala Ser

<210> 3
 <211> 420
 <212> DNA
 <213> MOUSE

<400> 3
 tcgtcccacg cgtccgcgcc aagcccgcgg cgcggaggac accgtgctcg gttccgggct 60
 gcggggacat tcccggacac acaccggagc agcagctgcg ccgcgacaca tctggagccg 120
 cgtaggatgt tcgtcaaate tgagactctg gagttgaagg aggaagagga ggtactgatg 180
 ctgctgggct cggtttcccc ggcctcggcg accctgaccc cgatgtcctc cagcgcggac 240
 gaggaggagg acgaggagct gcgccggccg ggctccgcgc gtgggcagcg tggagcggaa 300
 gccgggcagg ggggtgcagg cagtcgggcg tcgggtgcct ggggttgccg gacagggcgg 360
 ctgctatgca ctgtgcacga gtgctagcgt gtgccgtcgc gctcacgggc cgtctgcaga 420

<210> 4
 <211> 645
 <212> DNA
 <213> MOUSE

<400> 4
 atggcgctc atcccttggg tgcgtcacc atccaagtgt cccagagac acaacaacct 60
 ttcccggag cctcggacca cgaagtgtc agttccaatt ccacccacc tagccccact 120
 ctcataccta gggactgtc cgaagcagaa gtgggtgact gccgagggac ctcgaggaag 180
 ctccgcgcc gacgcggagg gcgcaacagg cccaagagcg agttggcact cagcaaacag 240

09980381.030602

cgaagaagcc ggcgcaagaa ggccaatgat cgggagcgca atcgcatgca caacctcaac 300
tcggcgctgg atgcgctgcg cgggtgtcctg cccaccttcc cggatgacgc caaacttaca 360
aagatcgaga ccctgcgctt cgcccacaac tacatctggg cactgactca gacgctgcgc 420
atagcggacc acagcttcta tggcccggag cccctgtgc cctgtggaga gctggggagc 480
cccggaggtg gctccaacgg ggactggggc tctatctact cccagtcctc ccaagcgggt 540
aacctgagcc ccacggcctc attggaggaa ttccctggcc tgcaggtgcc cagctcccca 600
tcctatctgc tcccgggagc actggtgttc tcagacttct tgtga 645

<210> 5
<211> 214
<212> PRT
<213> MOUSE

<400> 5

Met Ala Pro His Pro Leu Asp Ala Leu Thr Ile Gln Val Ser Pro Glu
1 5 10 15
Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
20 25 30
Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu
35 40 45
Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
50 55 60
Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
65 70 75 80
Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
85 90 95
His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
100 105 110
Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
115 120 125
His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
130 135 140
Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
145 150 155 160
Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
165 170 175
Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
180 185 190
Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu
195 200 205

09980381.030602

Val Phe Ser Asp Phe Leu
210

<210> 6
<211> 1412
<212> DNA
<213> MOUSE

<400> 6
cgtgctcggg tccgggctgc ggggacattc ccggacacac accggagcag cagctgcgcc 60
gcgacacatc tggagccgcg taggatgttc gtcaaactctg agactctgga gttgaaggag 120
gaagaggagg tactgatgct gctgggctcg gcttccccgg cctcggcgac cctgaccccc 180
atgtcctcca gcgcggacga ggaggaggac gaggagctgc gccggccggg ctccgcgcgt 240
gggcagcgtg gagcgggaagc cgggcagggg gtgcagggca gtccggcgctc ggggtgccggg 300
ggttgccggc cagggcggct gctgggcctg atgcacgagt gcaagcgctc cccgtcgcgc 360
tcacggggccg tctcccaggg tgccaagacg gcggagacgg tgcagcgcat caagaagacc 420
cgcaggctca aggccaacaa ccgcgagcgc aaccgcatgc acaacctaaa cgccgcgctg 480
gacgcgctgc gcgagggtgt gccaccttc cccgaggatg ccaagctcac gaagatcgag 540
acgctgcgct tcgcccacaa ttacatctgg gcgctcaccg agactctgcg cctggcggac 600
cactgcgccg gcgccggtgg cctccagggg gcgctcttca cggaggcggg gtcctgagc 660
ccgggagctg cgctcggcgc cagcggggac agcccttctc caccttcctc ctggagctgc 720
accaacagcc cggcgtcatc ctccaactcc acgtcccat acagctgcac tttatcgccc 780
gctagccccg ggtcagacgt ggactactgg cagccccac ctccggagaa gcatcgttat 840
gcgcctcacc tgcccctcgc cagggaactgt atctagagct gcgggtctcc ctctctcgtc 900
ctctacccgg ccctcttccc atccttctcc cgcctctcac cctccacgcc ccggactcca 960
cttcacagag cagagggtgg ccttgcaatc ccctcggcgg ctggtgcatt cgggggtgga 1020
gaccagctct ggtttattga agatgtgagg atttatggtc aaagaggact atggcgtgtg 1080
ggagtggggg ctggcgtggg gaacctcgta agactgtaaa agacactgag aaaaagtacc 1140
ataactaacg agtgtgcaga gcagactgac gtcctcccc tctctcagag ctgctggagg 1200
agaactccgg gcaggcagtt cgtgtgaatc tctcagaggg aatgcaactg gtccctgtga 1260
tcttttcacc ttcgtttcta catagagatg ttaatgtcag tcgaaagaaa tgtattttag 1320
catctgaatg aatttactgg taataatatt atccacacat ttgcaatggc tggcatctgc 1380
tctattccca ttgctgtctg caggctgtgg ga 1412

<210> 7
<211> 263

0980381.030602

<212> PRT
<213> MOUSE

<400> 7

Met Phe Val Lys Ser Glu Thr Leu Glu Leu Lys Glu Glu Glu Glu Val
1 5 10 15
Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro
20 25 30
Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
35 40 45
Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
50 55 60
Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
65 70 75 80
Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
85 90 95
Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
100 105 110
Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
115 120 125
Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
130 135 140
Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
145 150 155 160
Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
165 170 175
Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
180 185 190
Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
195 200 205
Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
210 215 220
Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
225 230 235 240
Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
245 250 255
Pro Leu Ala Arg Asp Cys Ile
260

<210> 8
<211> 1957
<212> DNA
<213> MOUSE

09980381.030602

<400> 8

gatacacaca gatctagagg ctccaggaga cgatgcgaca ctcagcctga aaagatttgg	60
aagatccaaa atgaaaactg attattgaat gaaattaaaa cctaaggtaa attaaggtta	120
aagaaccatg ttaacactac cgtttgacga gtctgtcgta atgcccgaat cccagatgtg	180
cagaaagttt gctagacaat gtgaggacca gaaacaaatt aagaaaccag agagctttcc	240
aaaacaagtt gtccttcgag gaaagagcat taaaagggcc cctggagaag aaaccgagaa	300
agaagaggag gaagaagaca gagaggaaga agatgagaat ggcttgtcca gaaggagggg	360
gctcaggaaa aaaaagacca ccaaactacg actggaaagg gtcaagttca ggagacagga	420
agctaattgcg cgcgagagga accggatgca cggcctcaat gatgctctgg acaatttgcg	480
aaaagtggtc ccctgttact ctaaaacca aaaactgtcc aaaatagaaa ctttacgact	540
ggccaaaaat tacatctggg cactttctga aattctgagg attggcaaga gaccggatct	600
gctcacgttc gtccaaaact tatgcaaagg tctttcccag ccaactacaa acttgggtggc	660
aggctgctta cagctcaacg ccagaagttt cctgatgggt caggggtggg aggctgcca	720
ccacacaagg tcaccctact ccacattcta cccaccctac cacagccctg agctggccac	780
tcccccaggg catgggactc ttgataattc caagtccatg aaaccctaca attactgcag	840
tgcatatgaa tccttctatg aaagtacctc ccctgagtgt gccagccctc agtttgaagg	900
tcccttaagt cctcccccaa ttaactataa tgggatattt tccctgaagc aagaagaaac	960
cttggactat ggcaaaaatt acaattatgg catgcattac tgtgcagtgc caccagggg	1020
tccccttggg caggggtgcca tggtcaggtt gccaccgac agccacttcc cttacgactt	1080
acatctgcgc agccaatctc tcactatgca agatgaatta aatgcagttt ttcataatta	1140
atgaggaaaa tgaaaataaa cagtggatcat tcacctcca ctctaattaa ggcaaagcag	1200
atgcttgtgg gctgcgtaat tggcacaact ctatctaagg tgtttactag tttctgaagt	1260
gtgtctcaaa gattgtgacc attttctatg tcataataaa tcccttttcg tatgagaact	1320
tcctttcctt ccctcttgtc tgtatcacac tgtgattctc tctctctctc tctctctctc	1380
tctctctctc tctctctctt actggcagaa tatttctttc ttgttttagt ttctttcaaa	1440
ttcacttaat ttgtttgaac aaggtgtcta agatgttgct gaataaagac atgcacacag	1500
catacttcaa tgtctatttc agttgtacag ttatgatgaa aatgcatgtt ataaaaatca	1560
gatgagtaaa atgtgtttat aattactagg attcatatat gtatctctga aatttttagt	1620
tttaaaatat taagagctaa ccatgaaatt aaaaggtgca tttggggatg cacaacggta	1680
tcaaaagcta tgcaattttc tgtttattag ggacaaaaat aagtgtattc agttggtaac	1740
aactattcct cttcaagcat tttcagagga ggaaacacgg tatttggggg aggttatcag	1800

0930301-030602

tgtcataatt tggggacaat taattcaatc atgaagaaaa aaaatattag cacttgtttt 1860
 gtattgttca ggatttttct gtacagggttt gttacagtgt ataattgtgt tttccatcct 1920
 acagtttataa agcaattataa catagatatatt tccactt 1957

<210> 9
 <211> 337
 <212> PRT
 <213> MOUSE

<400> 9

Met Leu Thr Leu Pro Phe Asp Glu Ser Val Val Met Pro Glu Ser Gln
 1 5 10 15

Met Cys Arg Lys Phe Ala Arg Gln Cys Glu Asp Gln Lys Gln Ile Lys
 20 25 30

Lys Pro Glu Ser Phe Pro Lys Gln Val Val Leu Arg Gly Lys Ser Ile
 35 40 45

Lys Arg Ala Pro Gly Glu Glu Thr Glu Lys Glu Glu Glu Glu Asp
 50 55 60

Arg Glu Glu Glu Asp Glu Asn Gly Leu Ser Arg Arg Arg Gly Leu Arg
 65 70 75 80

Lys Lys Lys Thr Thr Lys Leu Arg Leu Glu Arg Val Lys Phe Arg Arg
 85 90 95

Gln Glu Ala Asn Ala Arg Glu Arg Asn Arg Met His Gly Leu Asn Asp
 100 105 110

Ala Leu Asp Asn Leu Arg Lys Val Val Pro Cys Tyr Ser Lys Thr Gln
 115 120 125

Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Lys Asn Tyr Ile Trp
 130 135 140

Ala Leu Ser Glu Ile Leu Arg Ile Gly Lys Arg Pro Asp Leu Leu Thr
 145 150 155 160

Phe Val Gln Asn Leu Cys Lys Gly Leu Ser Gln Pro Thr Thr Asn Leu
 165 170 175

Val Ala Gly Cys Leu Gln Leu Asn Ala Arg Ser Phe Leu Met Gly Gln
 180 185 190

Gly Gly Glu Ala Ala His His Thr Arg Ser Pro Tyr Ser Thr Phe Tyr
 195 200 205

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr
 210 215 220

Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr
 225 230 235 240

Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe
 245 250 255

09980381.030602

Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser
 260 265 270
 Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly
 275 280 285
 Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala
 290 295 300
 Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu
 305 310 315 320
 Arg Ser Gln Ser Leu Thr Met Gln Asp Glu Leu Asn Ala Val Phe His
 325 330 335

Asn

<210> 10
 <211> 1056
 <212> DNA
 <213> MOUSE

<400> 10
 atgtcccgcc tgctgcatgc agaagagtgg gctgaggtaa aagagttggg ggaccaccat 60
 cgccatcccc agccgcacca cgtcccgccg ctgacgccac agccacctgc taccctgcag 120
 gcgagagacc ttcccgctcta cccggcagaa ctgtccctcc tggatagcac cgaccacgc 180
 gcttggtga ctccacttt gcagggcctc tgcacggcac gcgccgcca gtatctgctg 240
 cattctcccg agctgggtgc ctccgaggcc gcggcgcccc gggacgaggc tgacagccag 300
 ggtgagctgg taaggagaag cggctgtggc ggcctcagca agagccccgg gcccgtaaa 360
 gtacgggaac agctgtgcaa gctgaagggt ggggtttag tggacgagct tggctgcagc 420
 cgccagcgag ccccttccag caaacagggt aatgggtac agaagcaaag gaggctggca 480
 gcaaacgcaa gggaaacggcg caggatgcac gggctgaacc acgccttcga ccagctgcgc 540
 aacgttatcc cgtccttcaa caacgacaag aagctgtcca aatatgagac cctacagatg 600
 gccagatct acatcaacgc tctgtcggag ttgctgcaga ctcccaatgt cggagagcaa 660
 ccgccgccgc ccacagcttc ctgcaaaaat gaccaccatc accttcgcac cgcctcctcc 720
 tatgaaggag gtgcgggccc ctctgcggtg gctggggctc agccagcccc gggagggggc 780
 ccgagacctt ccccgcccg gccttgccgg actcgcttct caggcccagc ttcctctggg 840
 ggttactcgg tgcagctgga cgctttgcac ttcccagcct tcgaggacag ggccctaaca 900
 gcgatgatgg cacagaagga cctgtgcct tcgctgcccg ggggcatcct gcagcctgta 960
 caggaggaca acagcaaaac atctcccaga tcccacagaa gtgacggaga gttttcccc 1020
 cactctcatt acagtgactc tgatgaggcc agttag 1056

09900381.030602

<210> 11
<211> 351
<212> PRT
<213> MOUSE

<400> 11

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
1 5 10 15

Gly Asp His His Arg His Pro Gln Pro His His Val Pro Pro Leu Thr
20 25 30

Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Asp Leu Pro Val Tyr Pro
35 40 45

Ala Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp Leu Thr
50 55 60

Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu
65 70 75 80

His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu
85 90 95

Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu
100 105 110

Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu
115 120 125

Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala
130 135 140

Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala
145 150 155 160

Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe
165 170 175

Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu
180 185 190

Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu
195 200 205

Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro
210 215 220

Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser
225 230 235 240

Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala
245 250 255

Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg
260 265 270

Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala
275 280 285

0900201 030602

Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
 290 295 300
 Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val
 305 310 315 320
 Gln Glu Asp Asn Ser Lys Thr Ser Pro Arg Ser His Arg Ser Asp Gly
 325 330 335
 Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu Ala Ser
 340 345 350

<210> 12
 <211> 3261
 <212> DNA
 <213> MOUSE

<400> 12
 aatctatata tggcaaaaat gtatatgaaa tccaaggaca tgggtggagct ggtcaacaca 60
 caatcctgga tggacaaagg tctgagctct caaaatgaga tgaaggagca agagagaaga 120
 ccgggctctt atggaatgct cggaacctta actgaagagc atgacagtat tgaggaggat 180
 gaagaagagg aagaagatgg agataaacct aaaagaagag gtcccaagaa aaagaagatg 240
 actaaagctc gccttgaaag attcagggct cgaagagtca aggccaatgc tagagaacgg 300
 acccggatgc atggcctgaa tgatgccttg gataatctta ggagagtcac gccatgttac 360
 tctaaaactc aaaagctttc caagatagag actcttcgac tggcaaggaa ctacatctgg 420
 gccttgtctg aagtcttgga gactggtcag acacttgaag ggaagggatt tgtagagatg 480
 ctatgtaaag gtctctctca acccacaagc aacctgggtg ctggatgcct ccaactgggg 540
 cctcaatcta ccctcctgga gaagcatgag gaaaaatctt caatttgtga ctctactatc 600
 tctgtccaca gcttcaacta tcagtctcca gggctcccca gccctcctta tggccatatg 660
 gaaacacatt ctctccatct caagcctcaa ccatttaaga gtttgggtga ctcttttggg 720
 agccatccac ctgactgcag tccccccct tatgagggtc cactcacacc acccctgagc 780
 attagtggca acttctcctt aaagcaagac ggctcccctg atttggaata atcctacaat 840
 ttcattgccac attatacctc tgcaagtcta agttcagggc atgtgcattc aactcccttt 900
 cagactggca ctccccgcta tgatgttcct gtagacctga gctatgattc ctactccac 960
 catagcattg gaactcagct caatacgatc ttctctgatt agagcaataa gataagcacc 1020
 aatatttcag agaatgaagt ggagattttt ttcacatttc tagtggctga gctaaaactct 1080
 cagaaaattt aaaagaacct ttggatatgc atcaaacata atagtcctag tttgttcaga 1140
 acttctgtga cctgctaact ttcttcccat taacttctca cattggacca gtcctacatt 1200
 tggtaaactt aagtgaatat atttgatggg ttgaggccac atggtaatag aacagaaaga 1260

20990601 13E08660

aagcccaggc cctgttccaa tgggtgcaaaa gattaattga atgctctgcc aattaacttt	1320
ccatttccag tgttttttatt gctttctgat aaacatgaag caactgttcc aaatcaacat	1380
atacctttca cctcccacac atttttaaat ttaaaagcaa tcaaagcaaa tagcaaaaat	1440
ggaatgatta tacagaactg gaaggagcat caagtacatg tctgttggct tatagaatac	1500
aaaatttgtg tgaatttgac aaatcatctt tgtgtctatt taaatataac ttccagagcc	1560
taaaataata acttggatgt taccataaat aaccagtatg ttctttaaga gatcagctct	1620
acttattact gtgctgaaag gtatacacac cttttttagt gattggagaa ccatgataga	1680
agcctcacac aaactttatt ctttatacta tttaaaaaac aactgtctta gtactaggag	1740
acaagcaaga aagacattga aatttctctt ctggcacaca gaaatatcac ctagctcatt	1800
tcttagctcc cgtgactata gggctgtaga attttgcagg tattcaggtg cttcagttag	1860
aatcagaact cagccaggtt catactgtag agcaataaaa tgggtggttg ctgctatccc	1920
aactaacaca gttaaagaac tctgcctcac acatagccac tggaaaaatg tggatattct	1980
ccagcaagat gaatttcaact gtttaaagca atgcaattaa agccatagag tttcgtccac	2040
tccagtatca tatattccag aactgttgta atcaatcttg aattcttaca acataaatgc	2100
aactcettac ttcccaccta acactgattg ttatatgtc ttcaattcca agatattatg	2160
caattatatg caaaattttg attagaatca aaattaagag tcaatgaatc tgtctgtatc	2220
ttcaggacgg gttttgatca gttttaagaa agtttatttt cctttatgtg gcatctcttt	2280
tctttgtaac cacactgggt cagccaagtt tctcttctcc agagaaatta gctctgagaa	2340
attttactat catgatccat cttccacagc aattatttag gttcaactca agagtataca	2400
tagtttattt atagtgggtg aggatacacc tccaagaata aattttaaca acattaatga	2460
catatgaata tgccatttta tctaccaaac tatatatgta tctcttttct ttattgccct	2520
tatttatttc ttcacactga gagttatttt gtgtccatct tattgcagca cttactctgc	2580
tctactttgc acctttggat tataaatatg tttaaaagtc tgtaaagacg tcttaaacaa	2640
ctcgtgacag taattcacca cccctaagac cttgaatcac cctagtggaa ataggcaagg	2700
agaattattt atagaatcat cctatgtaat tttttttgag aatttgctct acctagcatt	2760
tatgtttata gataattgct atctgcatta tttattaggt tctatttatt taatttatct	2820
ttctttcttt ttatgtaaac atttgtgcc catagatata gcctcaaagc ttactggga	2880
aactagctta tatgtttgga gtgagagaaa aggagaaaat cagttcttga ttgcttgcaa	2940
tggttttata aaacagagca ataatttgaa tagatatgca acttaatggg tttagaattt	3000
ttcctttaag gtgcaacaga gttacattat ttttatgac tttggagaat gtagtacatg	3060
tgaaccagga ctgtaggctt gtgaagagag attttataat taaatacaaa tttagtactg	3120

09980381.030602

tactatgctt ggaaagaact tgttctttaa ataatgttta gtcttctggg agtgttttca 3180
gataaaatga agcaattgtt taaaagaaat ggctgttttc cctccctttt ccagtagcaa 3240
taaagctttg agtgttatta c 3261

<210> 13
<211> 501
<212> DNA
<213> ZEBRA FISH

<220>
<221> misc_feature
<222> (115)..(115)
<223> "n" can be any nucleotide

<400> 13
atgttaacgg taccgtttga agagccagat atgatgcgcg agtctcagtt tggcgccacg 60
ttcacgcgtc aggaagacgt ccggacactc agcagcgccg agctcaagga ggcanaggac 120
gacaacacgg acagggagga ggaggaggag agagaggagg actataacgg gctgccaaag 180
aagaagggtc cccgcaaaaa gaaatccgag ggacgcggtg accgagtcaa aatgcgccgt 240
caggaagcaa acgcgcgtga gcgcagccgc atgcacggtc taaacgacgc gctcgaaagc 300
ctgcgcaaag tcgtgccgtg ctactccaaa acgcagaaac tctccaagat cgaaaccctg 360
gggctgggca agaattacat ttgggctctg tctgagactt tgagcgcagg aaagcgacct 420
ggcctgcttg ggttggtagc aaccctgggc gtgggctggt ctagaggaca gaccagcttg 480
gtgggggagt gcctgcagct a 501

<210> 14
<211> 609
<212> DNA
<213> HUMAN

<400> 14
tttgacattg aattatgctg tgtgcatgtc tttattcaac agtatattct tagacacctt 60
gttcaaacaa attaaataag tttaaaagaa aattaaaaag aaaaaaatct ttccagtaga 120
aacagaatca cagtgttca cagacaaaag gaaaggaaaa gaagttctca tacgaaaaga 180
gatttattat tacatagaaa attctcacia tagttgaaac acacttcaga aactagtaaa 240
caccttagat agagttgtgc caattactca gccacaagc atctgctttg tcttaattag 300
acaggggagg tgaatgacca ctgtttatct tcattttcct cattaattat gaaaaactgc 360
atttaattca tcttgacattg tgagagattg gctgcgcaga tgtaagtcgt aagggaagtg 420
gctgtcggtg ggcaacctga acatggcacc ctgcccaagg ggaccctgg gtggcactgc 480

09980331-030602

acagtaatgc atgccgtaat tgtaattttt accatagtcc aaggtttctt cttgcttcag 540
ggaaaatatc ccattatagg taattggggg aggacttaag ggaccttcaa actgagggct 600
ggcacactc 609

<210> 15
<211> 675
<212> DNA
<213> HUMAN

<400> 15
tagagagcgg caggagacga tgcgacactc agcctgaaaa gatttggaag acccaaatg 60
aaaactgatt attgaatgaa attaaaacct aaggtaattt aagattagag aaccatgtta 120
aactaccgt ttgatgagtc tgttgtaatg ccagaatccc agatgtgcag aaagttttct 180
agagaatgcg aggaccagaa gcaaattaag aagccagaaa gcttttccaa acagattgtc 240
cttcgaggaa agagcatcaa aagggcccct ggagaagaaa ccgagaaaga agaagaggag 300
gaagacaggg aagaggaaga tgaaaatggg ttgcctagaa ggaggggtct taggaaaaaa 360
aagacaacaa agctgcgatt ggaaagggtc aagttcagga gacaggaagc gaacgcgcgc 420
gagaggaaca ggatgcacgg cctcaacgac gctctggaca acttaagaaa agtggtcgcg 480
tgttattcta tgaccagag actgtccaaa atagagactg tactactggc caaaaactac 540
atctgggcac tgtctgatat gctgagaatc ggcaagagac cagatctgct cacgattcgg 600
caaagctgat gcatagggtc ttgccagcca actacagact tgggtggcagg ctggtcgcag 660
ctcaacgaca ggagt 675

<210> 16
<211> 1476
<212> DNA
<213> DROSPHILA

<220>
<221> misc_feature
<222> (203)..(203)
<223> "n" can be any nucleotide

<220>
<221> misc_feature
<222> (217)..(217)
<223> "n" can be any nucleotide

<400> 16
ctccaccctc gtgtgccgtt gagcgtgaaa gtcacaaatt atgggcgaca gagggagagg 60
gagagagaga gaggggaaga tcccatggca tgatagtacc aatttggaac gatatgacgc 120
gtgcctggcg cgagagagat gacaacaggc gaagtgtagg cgtttcacca ccgagcgaaa 180

09930331.030602

gggagggaaa catatctaac ccntaagtca cccagntcc tcggggagat cctttggccg 240
 ggccatggta atagctgcga ggatcctggg gccaggggtc atttgcgggc catttacaca 300
 aacttgggtca gaacggcggt gaaaatattt gtagaatgca tctcgcgggg gttgaccgta 360
 gtcaagtctg gatccgatcg gatcgtttca gttgcaacga aactttcaag ccgcgcggat 420
 ctgcaatgag ctactactac tcgtctgcct ccgaggagga tggcagttcc cagtatctgg 480
 gcagtcccaa ctacaacttg acccagttgc cgccagtttc tggccaggat tacggacagg 540
 gggctttctt atcgccggaa tggcaattct tggatgccgc aggcggaaact caaacggaac 600
 taggacctat aatggagggtg caaggacagc acaccagcc gcagaccaa cggcgggagta 660
 acagctccac aggatcggac ggtaggaaga gcagtccaga gcagaccaat ctcagtccca 720
 cgggtccagaa gagaagacga caggctgcc aatgcgcggga aaggaagcgg atgaatggat 780
 taaatgcggc tttcgagcgc ctaagggaag tggtgccgc tccgtccatt gaccagaaat 840
 tgtccaagtt cgagactctc cagatggccc agtcctacat cctggcgctg tgcgatctcc 900
 tcaacaacgg ggacgtggaa gtggatgccg ctgcatacac catcttcggc gacagcgata 960
 gtggatttgg attgagcggg ggatccttgt catagatgga tgatactaga cttaaagtta 1020
 gtgattttct tcttactgta gattaagtta aatatgtaat gaaataaatt gaaatgttta 1080
 attgaatgct aaaaataatt tcaatttcaa aggcattatt catggaacgc atcgcttgat 1140
 tgtgaaccaa gtgttcaatc caaatgagc tactcatcta accctttcta ccaattataa 1200
 ccagcccact actatacaca gatccccaga ttcaattggc catcagatcg tttggctgcg 1260
 cctcaatgat ttcgaaaacg atcataaatt aattactcaa cagttcattg ataggcgtac 1320
 ttcaagtttt grtctaacc cgaacgattc cgaaactgcg aagccaccac agtgggcggt 1380
 gttagcgtgac acccctgaac tcctggccag aactcctctc attgaataaa aaaggcagct 1440
 gagtccttcg gcttcgggtg ggtgctgttt tttttt 1476

<210> 17
 <211> 189
 <212> PRT
 <213> DROSOPHILA

<400> 17

Met	Ser	Tyr	Tyr	Tyr	Ser	Ser	Ala	Ser	Glu	Glu	Asp	Gly	Ser	Ser	Gln
1				5				10					15		
Tyr	Leu	Gly	Ser	Pro	Asn	Tyr	Asn	Leu	Thr	Gln	Leu	Pro	Pro	Val	Ser
			20				25					30			
Gly	Gln	Asp	Tyr	Gly	Gln	Gly	Ala	Phe	Leu	Ser	Pro	Glu	Trp	Gln	Phe
		35					40					45			

09980381.030602

Leu Asp Ala Ala Gly Gly Thr Gln Thr Glu Leu Gly Pro Ile Met Glu
 50 55 60
 Val Gln Gly Gln His Thr Gln Pro Gln Thr Lys Arg Arg Ser Asn Ser
 65 70 75 80
 Ser Thr Gly Ser Asp Gly Arg Lys Ser Ser Pro Glu Gln Thr Asn Leu
 85 90 95
 Ser Pro Thr Val Gln Lys Arg Arg Arg Gln Ala Ala Asn Ala Arg Glu
 100 105 110
 Arg Lys Arg Met Asn Gly Leu Asn Ala Ala Phe Glu Arg Leu Arg Glu
 115 120 125
 Val Val Pro Ala Pro Ser Ile Asp Gln Lys Leu Ser Lys Phe Glu Thr
 130 135 140
 Leu Gln Met Ala Gln Ser Tyr Ile Leu Ala Leu Cys Asp Leu Leu Asn
 145 150 155 160
 Asn Gly Asp Val Glu Val Asp Ala Ala Ala Tyr Thr Ile Phe Gly Asp
 165 170 175
 Ser Asp Ser Gly Phe Gly Leu Ser Gly Gly Ser Leu Ser
 180 185

<210> 18
 <211> 1074
 <212> DNA
 <213> CHICKEN

<400> 18
 tttttccctt cccttttcct cgcggagccg cggccgcttt gccttcccct acagcgagga 60
 gctccgcttt ctctctatt tatttctaaa ccgttattgc ttaaccgcag ccccgaggagt 120
 gcctttccat gtgagtacgg gggacacagg cacctgcgat gcggtgcggc cgtgccaagc 180
 actcccaccc tccctccgtc cctccttggg gttacttttg gatatttttt ccctcccttt 240
 cccctcccc tcagcacctt cccccgctc cccctgccgc ccactgacgg ctccggcttc 300
 tctcccgag gatgcccgcg gaggcggcga gcagcggcgg cgtttcggag ccgcccggag 360
 ctccgcggga gcggcggagg agacgcggcc gtgcgcgggc gcggaccgag gctttgctgc 420
 acaccctcaa acggagccgc cgggtgaaag ccaacgaccg ggagcggaac cgcattgcacc 480
 acctcaagc cgcgtggat gagctccgca gcgtcctgcc gaccttcccc gacgacacca 540
 aactcaccaa aatcgaaacc ctgcgcttcg cttacaacta catctgggcc ctctccgaga 600
 cccttcgttt ggccgagcag tgcctccctc ctccccccgc ctccgcggg cccccgcgc 660
 ccccgagccc cggcagcgac gccggttcgt ggctgtccag cggttccccg gccgccccct 720
 cgctctgcgc ctccgcctcc ggccccagca gcccggccac ctccgaggac tgcggtacg 780
 tccctcgga cgcctgcgg gccttcgcg ggctgcccc cgcgcgcccg ggcgtccct 840

209060-1929660

gccgctagcc ctgcccgtgc gtgtctccgt cccccccac cttctccgta tcccgttgca 900
 cttttcagcc cctcccgccc ccagcccct ctctccgggg tgccctttcc cttcgccccc 960
 ccgcctcgtt ttccatacga cttgaaaaac ccggcaaaga aaagcgacag atttgctgcc 1020
 gcagacgagg tgaaaagtca attttacaat ttgtagctct ccggtgaaga aaaa 1074

<210> 19
 <211> 178
 <212> PRT
 <213> CHICKEN

<400> 19

Met Pro Ala Glu Ala Ala Ser Ser Gly Gly Val Ser Glu Pro Pro Gly
 1 5 10 15
 Ala Pro Arg Glu Arg Arg Arg Arg Arg Gly Arg Ala Arg Ala Arg Thr
 20 25 30
 Glu Ala Leu Leu His Thr Leu Lys Arg Ser Arg Arg Val Lys Ala Asn
 35 40 45
 Asp Arg Glu Arg Asn Arg Met His His Leu Asn Ala Ala Leu Asp Glu
 50 55 60
 Leu Arg Ser Val Leu Pro Thr Phe Pro Asp Asp Thr Lys Leu Thr Lys
 65 70 75 80
 Ile Glu Thr Leu Arg Phe Ala Tyr Asn Tyr Ile Trp Ala Leu Ser Glu
 85 90 95
 Thr Leu Arg Leu Ala Glu Gln Cys Leu Pro Pro Pro Pro Ala Phe Arg
 100 105 110
 Gly Pro Pro Ala Pro Pro Ser Pro Gly Ser Asp Ala Gly Ser Trp Leu
 115 120 125
 Ser Ser Gly Ser Pro Ala Ala Pro Ser Leu Cys Ala Ser Ala Ser Gly
 130 135 140
 Pro Ser Ser Pro Ala Thr Ser Glu Asp Cys Gly Tyr Val Pro Ser Asp
 145 150 155 160
 Ala Leu Arg Ala Phe Arg Gly Leu Pro Pro Ala Ala Pro Gly Ala Pro
 165 170 175

Cys Arg

<210> 20
 <211> 790
 <212> DNA
 <213> CHICKEN

<400> 20
 gcagccgccc ggccccggg ccgctccgac gccgccggg cgcgtgccag cgcccccca 60

09980381.030602

```

ccgcccgaacg gccgtcgacc agcggccgcg cccccctctc ccccgcccc gcaggatgcc      120
ggtgaaggcg gagagcccg cgcccgcggc ggaggacgaa ctgctgctgc tgcgcctcgc      180
ctcgcccgcc ccctcggcct cgctgccgtc cagcgccggc gaggaggacg aggacgagga      240
ggacggggcg cgcggcggc tgcaggagg cgctcggcg gcgggggcggc agcgagggcc      300
cccgcggggc gcgcgcacgc cggagacggc gcagcgcctc aagcggagcc ggcggctgaa      360
agccaacaac cgcgagcgca accgcatgca caacctgaac gcggcgctgg acgcgctgcg      420
cgacgtgctg cccaccttcc ccgaggacgc caagctcacc aagatcgaga cgctgcgctt      480
cgcccacaac tacatctggg cgctcaccga gacgtgcgc ctggccgggg ccgcccgcct      540
ggggggcgcc gccgacgcg cgcccggggc ggccgcccag ggcagcccct cgcccgccctc      600
gtcgtggagc ggcggcgcca gcccgcgcct ctcgcctcg ccctacgcct gcactttatc      660
gcccggcagc cccgcgggct ccgcctcgga cgccgagcac tggccgcccc cgcgggggcg      720
cttcgccccg ccgcgcgcgc cccaccgctg cctctaacgc ggcccgggcg gccctcgctc      780
ctccgacgtg                                     790

```

```

<210> 21
<211> 213
<212> PRT
<213> CHICKEN

```

```

<400> 21

```

```

Met Pro Val Lys Ala Glu Ser Pro Ala Pro Ala Ala Glu Asp Glu Leu
1          5          10          15
Leu Leu Leu Arg Leu Ala Ser Pro Ala Pro Ser Ala Ser Leu Pro Ser
20          25          30
Ser Ala Gly Glu Glu Asp Glu Asp Glu Glu Asp Gly Arg Pro Arg Arg
35          40          45
Leu Gln Glu Gly Ala Arg Arg Ala Gly Arg Gln Arg Gly Pro Pro Arg
50          55          60
Ala Ala Arg Thr Ala Glu Thr Ala Gln Arg Ile Lys Arg Ser Arg Arg
65          70          75          80
Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu Asn Ala
85          90          95
Ala Leu Asp Ala Leu Arg Asp Val Leu Pro Thr Phe Pro Glu Asp Ala
100         105         110
Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr Ile Trp
115         120         125
Ala Leu Thr Glu Thr Leu Arg Leu Ala Gly Ala Ala Arg Leu Gly Gly
130         135         140

```

209060-18E0860

Ala Ala Asp Ala Ala Pro Gly Ala Ala Ala Glu Gly Ser Pro Ser Pro
 145 150 155 160

Ala Ser Ser Trp Ser Gly Gly Ala Ser Pro Ala Pro Ser Ala Ser Pro
 165 170 175

Tyr Ala Cys Thr Leu Ser Pro Gly Ser Pro Ala Gly Ser Ala Ser Asp
 180 185 190

Ala Glu His Trp Pro Pro Pro Arg Gly Arg Phe Ala Pro Pro Pro Pro
 195 200 205

Pro His Arg Cys Leu
 210

<210> 22
 <211> 450
 <212> DNA
 <213> MOUSE

<400> 22
 atgaagtcgg cctgcaaacc ccacggccct ccggcgggag ctcgcggcgc gccccgtgc 60
 gcggggcgag ccgagcgcgc ggtctcgtgc gcggggcccg ggcggtgga gagcgcggcg 120
 cgcaggcgtc tggcggccaa cgcgcgcgag cggcgccgca tgcaggggct gaacacggcg 180
 ttcgaccggc tgcgcagggt ggtgccgcag tggggccagg acaagaagct gtccaagtac 240
 gagacactgc agatggcgct cagctacatc atcgcgctca cccgcaccc agccgaagcc 300
 gagcgggact gggtcgggct gcgctgcgag cagcggggcc gcgatcacc ctacctccct 360
 ttccggggtg ctaggctcca ggtagaccct gagccctatg ggagaggct cttcggcttc 420
 cagccggagc ccttcccat gccagctaa 450

<210> 23
 <211> 149
 <212> PRT
 <213> MOUSE

<400> 23

Met Lys Ser Ala Cys Lys Pro His Gly Pro Pro Ala Gly Ala Arg Gly
 1 5 10 15

Ala Pro Pro Cys Ala Gly Ala Ala Glu Arg Ala Val Ser Cys Ala Gly
 20 25 30

Pro Gly Arg Leu Glu Ser Ala Ala Arg Arg Arg Leu Ala Ala Asn Ala
 35 40 45

Arg Glu Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu
 50 55 60

Arg Arg Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr
 65 70 75 80

Glu Thr Leu Gln Met Ala Leu Ser Tyr Ile Ile Ala Leu Thr Arg Ile

09980381.030602

Leu Ala Glu Ala Glu Arg Asp Trp Val Gly Leu Arg Cys Glu Gln Arg
 100 105 110

Gly Arg Asp His Pro Tyr Leu Pro Phe Pro Gly Ala Arg Leu Gln Val
 115 120 125

Asp Pro Glu Pro Tyr Gly Gln Arg Leu Phe Gly Phe Gln Pro Glu Pro
 130 135 140

Phe Pro Met Ala Ser
 145

<210> 24
 <211> 861
 <212> DNA
 <213> MOUSE

<400> 24
 attcttttga gtcgggagaa ctaggtaaca attcggaaac tccaaagggg ggatgagggg 60
 cgcgcggggt gtgtgtgggg gatactctgg tccccctgac agtgacctct aagtcagagg 120
 ctggcacaca cacaccttcc attttttccc aaccgcagga tggcgctca tcccttgat 180
 gcgctcacca tccaagtgtc ccagagaca caacaacctt tccccggagc ctgggaccac 240
 gaagtgtca gttccaattc caccacact agcccaactc tcatacctag ggactgtctc 300
 gaagcagaag tgggtgactg ccgagggacc tcgaggaagc tccgcgcccg acgcggaggg 360
 cgcaacaggc ccaagagcga gttggcactc agcaaacagc gaagaagccg gcgcaagaag 420
 gccaatgatc gggagcgcaa tcgcatgcac aacctcaact cggcgctgga tgcgctgcgc 480
 ggtgtcctgc ccaccttccc ggatgacgcc aaacttacia agatcgagac cctgcgcttc 540
 gccacaaact acatctgggc actgactcag acgctgcgca tagcggacca cagcttctat 600
 ggcccggagc cccctgtgcc ctgtggagag ctggggagcc ccggaggtgg ctccaacggg 660
 gactggggct ctatctactc ccagttctcc caagcgggta acctgagccc cacggcctca 720
 ttggaggaat tccctggcct gcaggtgccc agctcccat cctatctgct cccgggagca 780
 ctggtgttct cagacttctt gtgaagagac ctgtctggct ctgggtggtg ggtgctagtg 840
 gaaagggagg ggaccacagc c 861

<210> 25
 <211> 214
 <212> PRT
 <213> MOUSE

<400> 25

Met Ala Pro His Pro Leu Asp Ala Leu Thr Ile Gln Val Ser Pro Glu
 1 5 10 15

09903031.030600

Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
 20 25 30
 Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu
 35 40 45
 Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
 50 55 60
 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
 65 70 75 80
 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
 85 90 95
 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
 100 105 110
 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
 115 120 125
 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
 130 135 140
 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
 145 150 155 160
 Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
 165 170 175
 Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
 180 185 190
 Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu
 195 200 205
 Val Phe Ser Asp Phe Leu
 210

<210> 26
 <211> 72
 <212> DNA
 <213> MOUSE

<400> 26
 atgcacgggc tgaatgcggc gctggacaac ccgagaaagg tggtaccttg ctactctaag 60
 acacagaagc tc 72

<210> 27
 <211> 24
 <212> PRT
 <213> MOUSE

<400> 27

Met His Gly Leu Asn Ala Ala Leu Asp Asn Pro Arg Lys Val Val Pro
 1 5 10 15

Cys Tyr Ser Lys Thr Gln Lys Leu

09980381-030602

<210> 28
 <211> 66
 <212> DNA
 <213> MOUSE

<400> 28
 atgcatggcc tgaatgatgc cttggataat cttagaagag tcatgccatg ttactctaaa 60
 actcaa 66

<210> 29
 <211> 22
 <212> PRT
 <213> MOUSE

<400> 29

Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg Val Met Pro
 1 5 10 15

Cys Tyr Ser Lys Thr Gln
 20

<210> 30
 <211> 1385
 <212> DNA
 <213> MOUSE

<400> 30
 cttaggaagc gccaaagcccg cggagcggag gacaccgtgc tcggttccgg gtgggggaca 60
 ttcccggaaca cacaccggag cagcagctgc gccggaacat tggagccgag taggtaagt 120
 tgcattccgc ggctttccat tcgcaggcag tgtccccacg caggctcacg ccgcccacgc 180
 taactccatc gtttagacgc agtgacttct gtgaccggca gaaggtggct cgagcccggg 240
 gcgctcctcc ccagctctgt cctcgccatc ttgcggaatg cacattgagg gagatggagg 300
 gggggggggcg gggcgcggcg ccagcgacac ttaccctgt ccattctggg aataaatttc 360
 atctgcctct tctttctcag gatgttcgtc aaatctgaga ctctggagtt gaaggaggaa 420
 gaggaggtac tgatgctgct gggctcggct tccccggcct cggcgaccct gaccccgatg 480
 tcctccagcg cggacgagga ggaggacgag gagctgcgcc ggccgggctc cgcgctggg 540
 cagcgtggag cggaagccga gcagggggtg cagggcagtc cggcgctcggg tgccgggggt 600
 tgccggccag ggcggctgct gggcctgatg cacgagtga agcgctcgcc gtcgctca 660
 cgggcccgtct cccgaggtgc caagacggcg gagacggtgc agcgcatcaa gaagaccgcg 720
 aggtcaagg ccaacaaccg cgagcgcaac cgcatgcaca acctaaacgc cgcgctggac 780
 gcgctgcgcg aggtgctgcc caccttcccc gaggatgcca agctcacgaa gatcgagacg 840
 ctgcgcttcg ccacaatta catctgggag ctcaccgaga ctctgcgcct ggcgggaccac 900

09980391.034502

tgcgccggcg ccggtggcct ccagggggcg ctcttcacgg aggcgggtgct cctgagccccg 960
 ggagctgcmc tcggcgccag cggggacagc ccttctccac cttcctcctg gagctgcacc 1020
 aacagccccg cgtcatcctc caactccacg tccccataca gctgcacttt atcgccccgt 1080
 agccccgggt cagacgtgga ctactggcag ccccccacctc cggagaagca tcgttatgcm 1140
 cctcacctgc ccctcgccag ggactgtatc tagagctgcm ggtctccctc tctcgtctcc 1200
 taccggggcc ctcttccca tccttctccc gccccccacc ctccacgccc cggaatccac 1260
 ttcacagaac agaagttggc cctttgcaat cccctccgcm gctgggtgctt cggggggttg 1320
 aaaacaactc tggtttattg aaattaagat tttggtcaaa aagaatatgc tttttggaat 1380
 tgggg 1385

<210> 31
 <211> 263
 <212> PRT
 <213> MOUSE

<400> 31

Met Phe Val Lys Ser Glu Thr Leu Glu Leu Lys Glu Glu Glu Glu Val
 1 5 10 15
 Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro
 20 25 30
 Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
 35 40 45
 Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Glu Gln Gly Val Gln
 50 55 60
 Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
 65 70 75 80
 Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
 85 90 95
 Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
 100 105 110
 Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
 115 120 125
 Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
 130 135 140
 Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
 145 150 155 160
 Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
 165 170 175
 Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser

0990031-030602

180

185

190

Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
 195 200 205

Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
 210 215 220

Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
 225 230 235 240

Tyr Trp Gln Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
 245 250 255

Pro Leu Ala Arg Asp Cys Ile
 260

<210> 32
 <211> 3541
 <212> DNA
 <213> MOUSE

<400> 32
 cagctgggca aggaaaatat gaaacacaag tgatctatat ccacagaata aacactaagt 60
 ttatgtgtct tttgacaagg tctcatgtag ctgagactgg ggttaaactt tttatgctac 120
 taaagataaa cttcaatatg ctaataaaga taaactcctg atttttctgc ttccacctct 180
 taaggcttgg gatcataggc atgtgccatc atgtctttct cagtttagat ttataccagg 240
 tattttgtgg tataacattt ttatattttc ctttttccag aatctataca tggcaaaaat 300
 gtatatgaaa tccaaggaca tgggtggagct ggtcaacaca caatcctgga tggacaaaagg 360
 tctgagctct caaaatgaga tgaaggagca agagagaaga ccgggctctt atggaatgct 420
 cggaacctta actgaagagc atgacagtat tgaggaggat gaagaagagg aagaagatgg 480
 agataaacct aaaagaagag gtcccaagaa aaagaagatg actaaagctc gccttgaaag 540
 attcagggct cgaagagtca aggccaatgc tagagaacgg acccgatgc atggcctgaa 600
 tgatgccttg gataatctta ggagagtcac gccatgttac tctaaaactc aaaagctttc 660
 caagatagag actcttcgac tggcaaggaa ctacatctgg gccttgctctg aagtcctgga 720
 gactggtcag acacttgaag ggaagggatt tntagagatg ctatgtaaag gtctctctca 780
 acccacaagc aacctgggtg ctggatgcct ccaactgggg cctcaatcta ccctcctgga 840
 gaagcatgag gaaaaatctt caatttgtga ctctactatc tctgtccaca gtttcaacta 900
 tcagtctcca gggctcccca gccctcctta tggccatatg gaaacacatt ctctccatct 960
 caagcctcaa ccatttaaga gtttgggtga ctcttttggg agccatccac ctgactgcag 1020
 tccccccct tatgaggggc cactcacacc acccctgagc attagtggca acttctcctt 1080
 aaagcaagac ggctcccttg atttgaaaa atcctacaat ttcatgccac attatacctc 1140

209060.TBEB55D

tgcaagtcta	agttcagggc	atgtgcattc	aactcccttt	cagactggca	ctccccgcta	1200
tgatgttcct	gtagacctga	gctatgattc	ctactcccac	catagcattg	gaactcagct	1260
caatacgatc	ttctctgatt	agagcaataa	gataagcacc	aatatttcag	agaatgaagt	1320
ggagatTTTT	ttcacatttc	tagtggctga	gctaaaactct	cagaaaattt	aaaagaacct	1380
ttggatatgc	atcaaacata	atagtcctag	tttgttcaga	acttcctgta	cctgctaact	1440
ttcttcccat	taactttctca	cattggacca	gtcctacatt	tggtaaactt	aagtgaatat	1500
atTTgatggT	ttgaggccac	atggtaatag	aacagaaaaga	aagcccaggc	cctgttccaa	1560
tggtgccaaa	gattaattga	atgctctgcc	aattaacttt	ccatttccag	tgTTTTtatt	1620
gctttctgat	aaacatgaag	caactgttcc	aatcaacat	atacctttca	cctcccacac	1680
atTTTTaaat	ttaaaagcaa	tcaaagcaaa	tagcaaaaat	ggaatgatta	tacagaactg	1740
gaaggagcat	caagtacatg	tctgttggct	tatagaatac	aaaatttgtg	tgaatttgac	1800
aaatcatctt	tgtgtctatt	taaatataac	ttccagagcc	taaaataata	acttggatgt	1860
taccataaat	aaccagtatg	ttctttaaga	gatcagctct	acttattact	gtgctgaaag	1920
gtatacacac	ctTTTTtagt	gattggagaa	ccatgataga	agcctcacac	aaactttatt	1980
ctttatacta	tttaaaaaac	aactgtctta	gtactaggag	acaagcaaga	aagacattga	2040
aattttctctt	ctggcacaca	gaaatatcac	ctagctcatt	tcttagctcc	cgTgactata	2100
gggctgtaga	atTTTgcagg	tattcaggTg	cttcagttag	aatcagaact	cagccaggTt	2160
catactgtag	agcaataaaa	tggTggtTg	ctgctatccc	aactaacaca	gttaaagaac	2220
tctgcctcac	acatagccac	tggaaaaatg	tggatattct	ccagcaagat	gaatttcact	2280
gtttaaagca	atgcaattaa	agccatagag	tttcgtccac	tccagtatca	tatattccag	2340
aactgttgta	atcaatcttg	aattcttaca	acataaatgc	aactccttac	ttcccaccta	2400
acactgattg	ttatattgtc	ttcaattcca	agatattatg	caattatatg	caaaattttg	2460
attagaatca	aaattaagag	tcaatgaatc	tgtctgtatc	ttcaggacgg	gttttgatca	2520
gttttaagaa	agtttatTTt	cttttatgtg	gcatctcttt	tctttgtaac	cacactggTt	2580
cagccaagTt	tctcttctcc	agagaaatta	gctctgagaa	atTTtactat	catgatccat	2640
cttccacagc	aattatttag	gttcaactca	agagtataca	tagtttattt	atagtgggtg	2700
aggatacacc	tccaagaata	aattTTtaaca	acattaatga	catatgaata	tgccattTTa	2760
tctaccaaac	tatatatgta	tctcttttct	ttattgccct	tatttatTTc	ttcacactga	2820
gagttattTT	gtgtccatct	tattgcagca	cttactctgc	tctactttgc	acctttggat	2880
tataaatatg	tttaaaagtc	tgtaaagacg	tcttaaacaa	ctcgtgacag	taattcacca	2940
cccctaagac	cttgaatcac	cctagtggaa	ataggcaagg	agaattattt	atagaatcat	3000

09960381-030602

cctatgtaat tttttttgag aatttgctct acctagcatt tatgtttata gataattgct 3060
atctgcatta tttattaggt tctatttatt taatttatct ttctttcttt ttatgtaaac 3120
atttgtgccc catagatata gcctcaaagc ttcactggga aactagctta tatgtttgga 3180
gtgagagaaa aggagaaaat cagttcttga ttgcttgcaa tggttttata aaacagagca 3240
ataatttgaa tagatatgca acttaatggg tttagaattt ttctttaag gtgcaacaga 3300
gttacattat tatttatgac tttggagaat gtagtacatg tgaaccagga ctgtaggctt 3360
gtgaagagag attttataat taaatacaaa tttagtactg tactatgctt ggaaagaact 3420
tgttctttta ataatgttta gtcttctggg agtgttttca gataaaatga agcaattgtt 3480
taaaagaaat ggctgttttc cctccctttt ccagtagcaa taaagctttg agtgttatta 3540
c 3541

<210> 33
<211> 330
<212> PRT
<213> MOUSE

<400> 33

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn
1 5 10 15

Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys
20 25 30

Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr
35 40 45

Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
50 55 60

Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
65 70 75 80

Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
85 90 95

Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
100 105 110

Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
115 120 125

Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
130 135 140

Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
145 150 155 160

Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
165 170 175

2099060" T8E08660

Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
 180 185 190
 Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
 195 200 205
 Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
 210 215 220
 Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240
 Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255
 Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270
 Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285
 Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300
 Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
 305 310 315 320
 Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

<210> 34
 <211> 800
 <212> DNA
 <213> MOUSE

<400> 34
 agggtagtag agtcactaat actacgtcct tgctgtgtag ttttctcagg ttttgattca 60
 ttttaagcat gggccaccaa tctcatgtac ctttttagct ttctttccaa gtgtgtctcc 120
 agttttctga cccccctcct gttttgctg ctctaccctg ccttgtagct ttctaatac 180
 aagtcttttc agttccctta gttttcacc atcaacttca gcagcccaca ccctctagtt 240
 ccttcctggt ttaaacaacaa acaaacacgc agtggcaaag ctggacctgg tcagagaagc 300
 cttgtgaagg aggtgtgtct ttaggctagg aaggggaggg gctaccctgt gggcaacatc 360
 tcccgccctg gtcagcagcc aaaaccagca aaacggcggc aagtcagaag ctccagtcag 420
 atcacaggag ctgcccagag actgtggtac tgaaagaact actcgcggga gctgaccccg 480
 ggaaagaggt actgaaaaga catagaaaac cagctgtggt ggaggcactg acatgaaggc 540
 atcctggtag tgcatacaga ctccaggaaa aagtagaata agtaacagcc aaggtactca 600
 gaccaggaac agtcactaga aggtagctac cagtttaaca tggacgactg aaagggtctt 660
 ctgtttccca cgatctgcct ggtcagggtca gggtagaact gactgctctg atagttcttc 720

209020-130360

aggacacaga ttagagttta atcttggaac tggacttcca gaggtgagcc tgtgaacggg 780
gtgtgggtac taaagtttct 800

<210> 35
<211> 515
<212> DNA
<213> CHICKEN

<400> 35
tttttctgta tgcgtgtgaa gctgcatctg caatagatat gaaaacctgt caatccagtc 60
atttggattc aggagtagaa tcagacatcc agtgcagaag tggatcaggc tgtgttgtga 120
agtgcagcac agaaagaatg gagagcgctg ccaagagaag actggctgcc aacgccaggg 180
agagaagacg gatgcaagga ctgaacacag cttttgatcg tttgaggaag gtggttccac 240
agtgggggtca agataagaag ctctccaaat atgagaccct tcagatggct ttgagttata 300
tcatggctct aacacgaata cttgctgaag cagagagata cagtactgaa agagaatgga 360
ttaaccttca ctgtgaacac ttatcatccag agagctacca ccattatacg ggacaaaaag 420
tggcaacaga cagtgatcct tatgcacagc gaatatcag ctatcacct gaacactttc 480
aaatagctaa ttagaactta ttacgagcta aaaaa 515

<210> 36
<211> 151
<212> PRT
<213> CHICKEN

<400> 36

Met	Lys	Thr	Cys	Gln	Ser	Ser	His	Leu	Asp	Ser	Gly	Val	Glu	Ser	Asp
1				5					10					15	
Ile	Gln	Cys	Arg	Ser	Gly	Ser	Gly	Cys	Val	Val	Lys	Cys	Ser	Thr	Glu
			20					25					30		
Arg	Met	Glu	Ser	Ala	Ala	Lys	Arg	Arg	Leu	Ala	Ala	Asn	Ala	Arg	Glu
		35					40					45			
Arg	Arg	Arg	Met	Gln	Gly	Leu	Asn	Thr	Ala	Phe	Asp	Arg	Leu	Arg	Lys
		50				55					60				
Val	Val	Pro	Gln	Trp	Gly	Gln	Asp	Lys	Lys	Leu	Ser	Lys	Tyr	Glu	Thr
65					70					75				80	
Leu	Gln	Met	Ala	Leu	Ser	Tyr	Ile	Met	Ala	Leu	Thr	Arg	Ile	Leu	Ala
			85						90					95	
Glu	Ala	Glu	Arg	Tyr	Ser	Thr	Glu	Arg	Glu	Trp	Ile	Asn	Leu	His	Cys
			100					105					110		
Glu	His	Phe	His	Pro	Glu	Ser	Tyr	His	His	Tyr	Thr	Gly	Gln	Lys	Val
		115					120					125			

09580341-03050

<210> 38
 <211> 263
 <212> PRT
 <213> MOUSE

<400> 38

```

Met Phe Val Lys Ser Glu Thr Leu Glu Leu Lys Glu Glu Glu Glu Val
1      5      10      15

Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro
      20      25      30

Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
      35      40      45

Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
      50      55      60

Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
65      70      75      80

Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
      85      90      95

Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
      100     105     110

Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
      115     120     125

Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
      130     135     140

Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
145      150      155      160

Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
      165      170      175

Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
      180      185      190

Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
      195     200     205

Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
      210     215     220

Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
225      230      235      240

Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
      245     250     255

Pro Leu Ala Arg Asp Cys Ile
      260

```

<210> 39
 <211> 938
 <212> DNA

09980381-030607

<400>	39					
cttatagggc	tcgagcggcc	gcccgggcag	gtcagggtgta	agaagagaaa	tcttcccagg	60
caaaatatcc	gtccctgtat	ccatagccac	aaactttcct	cccaaaagca	caaaccaaca	120
gaatggatgg	aatgagcacg	gatacaagag	aggtggttga	actcgacgtc	cagcattcga	180
gcttggggcg	gggggagcag	agcaagtacc	caccagcctt	ggcactcatg	gccagcagtg	240
accacgcgc	ctggctggct	cccgtgcagg	ctggcacctg	cgcggcacac	gccgaatacc	300
tgctgcactc	gcccggctcg	agcgcggaag	gcgtgtcctc	tgctccaac	ttcaggaaga	360
gcagcaagag	tcctgtcaaa	gtacgcgagc	tctgccggct	taaaggagct	gtgggggcag	420
atgagggcag	acagcgggcc	ccatccagca	aatccaccaa	cgtcgtgcag	aaacagaggc	480
gaatggctgc	caatgcccg	gagaggcgaa	gaatgcacgg	attgaaccac	gcgttcgacg	540
agctgcgcag	tgtcatccca	gcctttgaca	acgacaagaa	actctccaag	tacgaaaccc	600
tgcatatggc	ccagatctac	atcaacgccc	tgtccgactt	actacagggc	cccggtgcta	660
aagccgaccc	gccaaactgc	gacctgctgc	atgccaaacgt	gtagaaaacg	gaccgatctc	720
ccagaggatc	accgggcgtc	tgtcggagag	gcacgggcgt	gggttaccgc	taccagtacg	780
aggacggaac	attcaactct	ttcatggagc	aagacctcca	gtcgccctct	ggaacgagca	840
agtctggttc	ggaggccagt	aaagactcgc	ctcggtcgaa	ccggagtgat	ggagaagttc	900
tcgcctcact	gaagtgcgag	tgaacacctg	ccgggcgcg			938

<400> 40

Met	Asp	Gly	Met	Ser	Thr	Asp	Thr	Arg	Glu	Val	Val	Glu	Leu	Asp	Val
1				5					10					15	
Gln	His	Ser	Ser	Leu	Gly	Arg	Gly	Glu	Gln	Ser	Lys	Tyr	Pro	Pro	Ala
			20					25					30		
Leu	Ala	Leu	Met	Ala	Ser	Ser	Asp	Pro	Arg	Ala	Trp	Leu	Ala	Pro	Val
		35					40					45			
Gln	Ala	Gly	Thr	Cys	Ala	Ala	His	Ala	Glu	Tyr	Leu	Leu	His	Ser	Pro
	50					55					60				
Gly	Ser	Ser	Ala	Glu	Gly	Val	Ser	Ser	Ala	Ser	Asn	Phe	Arg	Lys	Ser
65					70					75					80
Ser	Lys	Ser	Pro	Val	Lys	Val	Arg	Glu	Leu	Cys	Arg	Leu	Lys	Gly	Ala
				85					90					95	

Val Gly Ala Asp Glu Gly Arg Gln Arg Ala Pro Ser Ser Lys Ser Thr
100 105 110

Asn Val Val Gln Lys Gln Arg Arg Met Ala Ala Asn Ala Arg Glu Arg
115 120 125

Arg Arg Met His Gly Leu Asn His Ala Phe Asp Glu Leu Arg Ser Val
130 135 140

Ile Pro Ala Phe Asp Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu
145 150 155 160

Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu Ser Asp Leu Leu Gln Gly
165 170 175

Pro Gly Ala Lys Ala Asp Pro Pro Asn Cys Asp Leu Leu His Ala Asn
180 185 190

Val Leu Glu Thr Asp Arg Ser Pro Arg Gly Ser Pro Gly Val Cys Arg
195 200 205

Arg Gly Thr Gly Val Gly Tyr Pro Tyr Gln Tyr Glu Asp Gly Thr Phe
210 215 220

Asn Ser Phe Met Glu Gln Asp Leu Gln Ser Pro Ser Gly Thr Ser Lys
225 230 235 240

Ser Gly Ser Glu Ala Ser Lys Asp Ser Pro Arg Ser Asn Arg Ser Asp
245 250 255

Gly Glu Val Leu Ala Ser Leu Lys Cys Glu
260 265

<210> 41
<211> 948
<212> DNA
<213> FROG

<400> 41
atgtcagaga tggatcaatgt gcatgggtgg atggaggaag cccttagttc ccaggatgag 60
atgaaggaga ggaatcagtc tgcctatgat atcatttcag gtctatgccca tgaggaaagg 120
ggcagcattg atggagaaga ggatgatgaa gaagaagagg atggagagaa accaaaaaag 180
aggggaccca aaaaaaagaa gatgaccaag gctagagtgg agagggtccg tgtccgtaga 240
gtaaaagcca atgccaggga gcgttcaaga atgcatggac ttaatgatgc cctggaaaat 300
ttgagaaggg ttatgccttg ctattccaaa acacaaaagt tgtctaaaat tgagactctt 360
agactggcca gaaactatat atgggcatta tctgatattc tagaacaagg tcaaaatgca 420
gagggaaagg gctttctgga aatactctgc aaagggtctt ctcagccaac aagcaactta 480
gtagctggct gcttgcaact tggacctcag gccatgttct tggataaaca cgaagaaaag 540
tctcatatat gtgattcctc tcttactggg catacttata attaccagtc cccaggacta 600
cccagtcctc cttatggtaa cattgatgtt caccacttgc acttgaaacc ctcttctttc 660

0098031.030602

aaaccagtaa tggatccttc tgtggtaacc catacactta actgtaccac tccaccatat 720
 gaaggagctc taacacctcc actcagcatc ggtggtaatt tttctttgaa gcaagatagt 780
 tcacccgata tggataaaatc atatgcattc aggtccccct atccagctct tgggcttggt 840
 ggatctcatg gacatgcgtc acactttcat accagtgttc caaggatatga actaccata 900
 gacatggctt acgagcctta cccacaccat gctatatattca ctgaataa 948

<210> 42
 <211> 315
 <212> PRT
 <213> FROG

<400> 42

Met	Ser	Glu	Met	Val	Asn	Val	His	Gly	Trp	Met	Glu	Glu	Ala	Leu	Ser
1				5					10					15	
Ser	Gln	Asp	Glu	Met	Lys	Glu	Arg	Asn	Gln	Ser	Ala	Tyr	Asp	Ile	Ile
			20					25					30		
Ser	Gly	Leu	Cys	His	Glu	Glu	Arg	Gly	Ser	Ile	Asp	Gly	Glu	Glu	Asp
		35					40					45			
Asp	Glu	Glu	Glu	Glu	Asp	Gly	Glu	Lys	Pro	Lys	Lys	Arg	Gly	Pro	Lys
	50					55					60				
Lys	Lys	Lys	Met	Thr	Lys	Ala	Arg	Val	Glu	Arg	Phe	Arg	Val	Arg	Arg
65					70					75					80
Val	Lys	Ala	Asn	Ala	Arg	Glu	Arg	Ser	Arg	Met	His	Gly	Leu	Asn	Asp
				85					90					95	
Ala	Leu	Glu	Asn	Leu	Arg	Arg	Val	Met	Pro	Cys	Tyr	Ser	Lys	Thr	Gln
			100					105					110		
Lys	Leu	Ser	Lys	Ile	Glu	Thr	Leu	Arg	Leu	Ala	Arg	Asn	Tyr	Ile	Trp
		115					120					125			
Ala	Leu	Ser	Asp	Ile	Leu	Glu	Gln	Gly	Gln	Asn	Ala	Glu	Gly	Lys	Gly
		130				135					140				
Phe	Leu	Glu	Ile	Leu	Cys	Lys	Gly	Leu	Ser	Gln	Pro	Thr	Ser	Asn	Leu
145					150					155					160
Val	Ala	Gly	Cys	Leu	Gln	Leu	Gly	Pro	Gln	Ala	Met	Phe	Leu	Asp	Lys
				165					170					175	
His	Glu	Glu	Lys	Ser	His	Ile	Cys	Asp	Ser	Ser	Leu	Thr	Gly	His	Thr
			180					185					190		
Tyr	Asn	Tyr	Gln	Ser	Pro	Gly	Leu	Pro	Ser	Pro	Pro	Tyr	Gly	Asn	Ile
		195					200					205			
Asp	Val	His	His	Leu	His	Leu	Lys	Pro	Ser	Ser	Phe	Lys	Pro	Val	Met
	210					215					220				
Asp	Pro	Ser	Val	Val	Thr	His	Thr	Leu	Asn	Cys	Thr	Thr	Pro	Pro	Tyr

0960361.030602

taattggcac aactctatct aaggtgttta ctagtctctg aagtgtgttt caaagattgt 1200
 gaccattttc tatgtcataa taaatccctt ttcgtatgag aacttccttt ccttcctctt 1260
 tgtctgtatc aactgtgat tctctctctc tctctctctc tctctctctc tctctctctc 1320
 tcttactggc agaataatttc tttcttggtt tagtttcttt caaattcact taatttggtt 1380
 gaacaagggtg tctaagatgt tgctgaataa agacatgcac acagcatact tcaatgtcta 1440
 tttcagttgt acagttatga tgaaaaatgca tgttataaaa atcagatgag taaaatgtgt 1500
 ttataattac taggattcat atatgtatct ctgaaatttt agttttttaa 1550

<210> 44
 <211> 337
 <212> PRT
 <213> MOUSE

<400> 44

Met	Leu	Thr	Leu	Pro	Phe	Asp	Glu	Ser	Val	Val	Met	Pro	Glu	Ser	Gln
1				5					10					15	
Met	Cys	Arg	Lys	Phe	Ala	Arg	Gln	Cys	Glu	Asp	Gln	Lys	Gln	Ile	Lys
			20					25					30		
Lys	Pro	Glu	Ser	Phe	Pro	Lys	Gln	Val	Val	Leu	Arg	Gly	Lys	Ser	Ile
		35					40					45			
Lys	Arg	Ala	Pro	Gly	Glu	Glu	Thr	Glu	Lys	Glu	Glu	Glu	Glu	Glu	Asp
	50					55				60					
Arg	Glu	Glu	Glu	Asp	Glu	Asn	Gly	Leu	Ser	Arg	Arg	Arg	Gly	Leu	Arg
65					70				75					80	
Lys	Lys	Lys	Thr	Thr	Lys	Leu	Arg	Leu	Glu	Arg	Val	Lys	Phe	Arg	Arg
			85					90						95	
Gln	Glu	Ala	Asn	Ala	Arg	Glu	Arg	Asn	Arg	Met	His	Gly	Leu	Asn	Asp
			100					105					110		
Ala	Leu	Asp	Asn	Leu	Arg	Lys	Val	Val	Pro	Cys	Tyr	Ser	Lys	Thr	Gln
		115					120					125			
Lys	Leu	Ser	Lys	Ile	Glu	Thr	Leu	Arg	Leu	Ala	Lys	Asn	Tyr	Ile	Trp
	130					135					140				
Ala	Leu	Ser	Glu	Ile	Leu	Arg	Ile	Gly	Lys	Arg	Pro	Asp	Leu	Leu	Thr
145					150				155						160
Phe	Val	Gln	Asn	Leu	Cys	Lys	Gly	Leu	Ser	Gln	Pro	Thr	Thr	Asn	Leu
				165					170					175	
Val	Ala	Gly	Cys	Leu	Gln	Leu	Asn	Ala	Arg	Ser	Phe	Leu	Met	Gly	Gln
			180					185					190		
Gly	Gly	Glu	Ala	Ala	His	His	Thr	Arg	Ser	Pro	Tyr	Ser	Thr	Phe	Tyr
		195					200					205			

09980381-030602

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr
 210 215 220
 Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr
 225 230 235 240
 Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe
 245 250 255
 Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser
 260 265 270
 Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly
 275 280 285
 Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala
 290 295 300
 Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu
 305 310 315 320
 Arg Ser Gln Ser Leu Thr Met Gln Asp Glu Leu Asn Ala Val Phe His
 325 330 335

Asn

<210> 45
 <211> 1393
 <212> DNA
 <213> MOUSE

<400> 45
 aagcttcggt gcacgcgacc tgggtgtgcga tctccgagtg agagggggag ggtcagagga 60
 ggaaggaaaa aaaatcagac cttgcagaag agactaggaa ggtttttgtt gttgttgttc 120
 ggggcttata cccttcggtt aactgggttg ccagcacctc ctctaacacg gcacctccga 180
 gccattgcag tgcgatgtcc cgctgtctgc atgcagaaga gtgggctgag gtaaaagagt 240
 tgggggacca ccacgccat cccagccgc accacgtccc gccgctgacg ccacagccac 300
 ctgctaccct gcaggcgaga gaccttcccg tctaccggc agaactgtcc ctctggata 360
 gcaccgacc acgcgcctgg ctgactccca ctttgcaggg cctctgcacg gcacgcgccg 420
 cccagtatct gctgcattct cccgagctgg gtgcctccga ggccgcggcg ccccgggacg 480
 aggctgacag ccagggtgag ctggtaagga gaagcggctg tggcggcctc agcaagagcc 540
 ccgggcccgt caaagtacgg gaacagctgt gcaagctgaa ggggtggggtt gtagtggacg 600
 agcttggctg cagccgccag cgagcccctt ccagcaaaca ggtgaatggg gtacagaagc 660
 aaaggaggct ggcagcaaac gcaagggaac ggcgcaggat gcacgggctg aaccacgcct 720
 tcgaccagct gcgcaacgtt atcccgctct tcaacaacga caagaagctg tccaaatatg 780
 agaccctaca gatggcccag atctacatca acgctctgtc ggagttgctg cagactccca 840

09980381.030602

atgtcggaga gcaaccgccc ccgcccacag cttcctgcaa aaatgaccac catcaccttc 900
gcaccgcctc ctccatgaa ggaggtgagg gcgcctctgc ggtagctggg gctcagccag 960
ccccgggagg gggcccgaga cctaccccgcc ccgggccttg ccggactcgc ttctcaggcc 1020
cagcttcttc tgggggttac tcggtgcagc tggacgcttt gcacttccca gccttcgagg 1080
acagggccct aacagcgatg atggcacaga aggacctgtc gccttcgctg cccgggggca 1140
tcctgcagcc tgtacaggag gacaacagca aaacatctcc cagatccac agaagtgcg 1200
gagagttttc cccccactct cattacagtg actctgatga ggccagttag gaaggcaaca 1260
gtccctgaa aactgagaca accaaatgcc cttcctagcg cgcggaagc cccgtgacaa 1320
atatccctgc accctttaat ttttggtctg tggatgctg tgtagcaac gacttgactt 1380
cggacggctg cag 1393

<210> 46
<211> 351
<212> PRT
<213> MOUSE

<400> 46

Met	Ser	Arg	Leu	Leu	His	Ala	Glu	Glu	Trp	Ala	Glu	Val	Lys	Glu	Leu
1			5						10					15	
Gly	Asp	His	His	Arg	His	Pro	Gln	Pro	His	His	Val	Pro	Pro	Leu	Thr
			20					25						30	
Pro	Gln	Pro	Pro	Ala	Thr	Leu	Gln	Ala	Arg	Asp	Leu	Pro	Val	Tyr	Pro
			35				40					45			
Ala	Glu	Leu	Ser	Leu	Leu	Asp	Ser	Thr	Asp	Pro	Arg	Ala	Trp	Leu	Thr
		50				55					60				
Pro	Thr	Leu	Gln	Gly	Leu	Cys	Thr	Ala	Arg	Ala	Ala	Gln	Tyr	Leu	Leu
65					70				75					80	
His	Ser	Pro	Glu	Leu	Gly	Ala	Ser	Glu	Ala	Ala	Ala	Pro	Arg	Asp	Glu
			85					90						95	
Ala	Asp	Ser	Gln	Gly	Glu	Leu	Val	Arg	Arg	Ser	Gly	Cys	Gly	Gly	Leu
			100					105					110		
Ser	Lys	Ser	Pro	Gly	Pro	Val	Lys	Val	Arg	Glu	Gln	Leu	Cys	Lys	Leu
			115				120					125			
Lys	Gly	Gly	Val	Val	Val	Asp	Glu	Leu	Gly	Cys	Ser	Arg	Gln	Arg	Ala
			130			135					140				
Pro	Ser	Ser	Lys	Gln	Val	Asn	Gly	Val	Gln	Lys	Gln	Arg	Arg	Leu	Ala
145					150					155					160
Ala	Asn	Ala	Arg	Glu	Arg	Arg	Arg	Met	His	Gly	Leu	Asn	His	Ala	Phe
				165					170					175	

09980381.030600

tctctccatc tcaagcctca accattttaag agtttgggtg actcttttgg gagccatcca 720
cctgactgca gtaccccccc ttatgagggt ccactcacac caccctgag cattagtggc 780
aacttctcct taaagcaaga cggctcccct gatttgga aaacctacaa tttcatgcca 840
cattatacct ctgcaagtct aagttcaggg catgtgcatt caactccctt tcagactggc 900
actccccgct atgatgttcc tgtagacctg agctatgatt cctactccca ccatagcatt 960
ggaactcagc tcaatacgat cttctctgat tag 993

<210> 48
<211> 330
<212> PRT
<213> MOUSE

<400> 48

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn
1 5 10 15
Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys
20 25 30
Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr
35 40 45
Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
50 55 60
Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
65 70 75 80
Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
85 90 95
Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
100 105 110
Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
115 120 125
Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
130 135 140
Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
145 150 155 160
Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
165 170 175
Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
180 185 190
Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
195 200 205
Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
210 215 220

09980381.030602

Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240
 Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255
 Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270
 Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285
 Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300
 Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
 305 310 315 320
 Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

<210> 49
 <211> 2264
 <212> DNA
 <213> FROG

<400> 49
 gacagtcagt agatgctcct ttcccaaagt gtatcttgca gtagccttac actaatactg 60
 cctgtcttgt agctggagag ctttgtatcg atgctaagag cactgggtat ctacaaagag 120
 gatcactgca tatgaatgga ataaggagtg ctgctgctac ccaggctggg gtttgttccg 180
 agcccttcaa aaccttttgg ccatagaatc actgtgttga catgaagtca gattcaccag 240
 tgcatgggga gtcccatact gaatgccagt caccatgccc actaagttgc atgccagcca 300
 ggctggaagg ctctaccaag agacgtctgg ctgccaatgc cagggaaaga aggagaatgc 360
 aaggactgaa taccgccttc gatagtctga ggaaagttgt accgcaatgg ggtgaggaca 420
 aaaaactttc caagtatgag actctacaga tggcactgag ctacatcatg gcactaagca 480
 ggatcctcac ggaagcagaa agatacagca gaactgatcc aggggaatgg actaaaatgc 540
 actttgatca cattcaggaa gaacagtgcc tcagttatat gggagtgaga tgcccaagag 600
 actgtgatcg ctacctgccc cagacttttt ctactagga taggagatgt gagcaacagt 660
 cagcaggcaa ggtactatag acctgaagat agcagtgtat tcctacacac agcagccaat 720
 aatacaggga catttgcac atgggttatt tgtcatgtca ttctgccc aa tgactgctt 780
 atttcattaa gcacccaaag tcccaggact gggaatatat gtagggcacc ccacgtgatg 840
 cagcccaaag tatgtgctgc tgcaactgat agtgagctgt gggacactgg aaaagcaaag 900
 tgcgctggta ttttgtaa at gaaaatgtca ttatgggtgg catataataa ttacttacac 960
 acagcacagt tatataattt cattgctgtt agaaagcccc tttgtctctt acccccac 1020

0900381.030502

Met	Lys	Ser	Asp	Ser	Pro	Val	His	Gly	Glu	Ser	His	Thr	Glu	Cys	Gln
1				5					10					15	
Ser	Pro	Cys	Pro	Leu	Ser	Cys	Met	Pro	Ala	Arg	Leu	Glu	Gly	Ser	Thr
			20					25					30		
Lys	Arg	Arg	Leu	Ala	Ala	Asn	Ala	Arg	Glu	Arg	Arg	Arg	Met	Gln	Gly
		35					40					45			
Leu	Asn	Thr	Ala	Phe	Asp	Ser	Leu	Arg	Lys	Val	Val	Pro	Gln	Trp	Gly

50

55

60

Glu Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Thr Glu Ala Glu Arg Tyr Ser
85 90 95

Arg Thr Asp Pro Gly Glu Trp Thr Lys Met His Phe Asp His Ile Gln
100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Gly Val Arg Cys Pro Arg Asp Cys
115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
130 135

<210> 51

<211> 2123

<212> DNA

<213> FROG

<400> 51

gacagtcagt agatgctcct tgcctgaagt gtatcttgca gtagccttac actgccttgt 60
agctggagag ccttgatatca ctgctaaca cactgggtat caacaaagaa gacaactgca 120
taaaaatgaa ataaggagat actaccaggt ctgggggttta ttttgagtct ttcagaactt 180
tctagggata gaatatctct gctgacatga agtcagattc accagtgcac agggagtccc 240
atactggatg ccagtcacca tgcccactaa ggtgcttgcc agccaggctg gaaggctcta 300
ccaagagacg tctggctgcc aatgccagag aaaggaggag aatgcaagga ctaaataaccg 360
ccttcgatag totgaggaaa gttgtaccac aatggggtga agacaaacaa ctttccaaat 420
atgagactct gcagatggcg ctgagctaca tcatggcact gagcaggatc ctctcggaag 480
cagagaggta cagcaggact gatccagagg aatggactaa tattcaatat gatcacattg 540
aggaggagca gtgcctcagt tatatggagg tgagatgcc aagagactgt gatcgttacc 600
tgccccagac tttttctcac taggataaga gcaggcaagg tactactgac ctgaagacag 660
cactgtttta atataatggg tcggttatac agcacccaat gatacaggga catttgcac 720
atgggctatt tgtcatgttg tttttcccaa tgcaatgctt atttccttaa gcaccctacg 780
ttcaggactg ggtacatatg tagggaaccc caagtgatgc agcccagagg atgcggtgct 840
gcaacggatg gcagttagtg agctgtggaa cactggaaaa gccaaagtga ctggtatttt 900
gtgaaaggac atgcaagtta ttatgggtgg catataatat ttacctccat acagcacagt 960
gatataactt cattgcctcc atcatacctg tgtgattata tataaaatgg tagttcctga 1020
gtcactactt tccatgttac ttatgcactg ttatcagata acatagagaa agtagtattt 1080
atacattaga aaaagtacta tatgtgcata taaattggcg tttaaagcag tctggataaa 1140

09980381.030602

tcattttctg tggactcttt tcttacccca aggagccatt tatagtttaa gtgctgctat 1200
aggcactgct cataagggaa aggaaacatt tttgtcactt gctgataata caaattgcat 1260
tctacaccag aattcttaat taactatact gtctagttaa cagaaaggtc taaattaaaa 1320
tcaacaagag gtataattta catattttac cattttctgg ctctctgtctg ccttttgaga 1380
gtggcaaatt acaacgtata taaaattcct acagggtctca atctacttgt tgctgtaaag 1440
acaaaccttg gtgtattttt aaggaaacct taagtaattc ttttggttag tatacatttc 1500
ttaaataattt ttatttgtaa tgggcgtcaa ttgtttattt gttaaagcag ctccaaaaat 1560
agcagatatg cttgtatttt tcagggtatgc aaatgggtatt tcagcctata ttgggaaagc 1620
agtaagcaaa tctttgtaat tgaaattgta gtaaaactga acatatgggtg aattgcttgg 1680
caatgtactg tatacatgct gacctataag ggctatgtag caaagttggg aaaaagtttt 1740
ccctatcaaa atcactgcag gtttattggg ttgttgacaga tagaataata aaatctgaca 1800
ttgctgatgt gggtaaggta ttttattccc catttaatat cttaatcttt cttcttacac 1860
tgaaaacatt actagcccct tgccaatgta ttcttatctg tcaaattcag gagttcatga 1920
gacttacctg tacataatcc ctatgaaacc aagacaatgt gtggggaata agaggatttg 1980
ctgcacaaat tagggcagag atacatggtc tgactgtgac aaatctcttc ttcttcggag 2040
cgtttaatat ccccaaactg cctttccagg cactttgttc tccgaagtcg cccgaagttg 2100
cctaacgagg caacttcagc acg 2123

<210> 52
<211> 138
<212> PRT
<213> FROG

<400> 52

Met Lys Ser Asp Ser Pro Val His Arg Glu Ser His Thr Gly Cys Gln
1 5 10 15
Ser Pro Cys Pro Leu Arg Cys Leu Pro Ala Arg Leu Glu Gly Ser Thr
20 25 30
Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly
35 40 45
Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly
50 55 60
Glu Asp Lys Gln Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
65 70 75 80
Tyr Ile Met Ala Leu Ser Arg Ile Leu Ser Glu Ala Glu Arg Tyr Ser
85 90 95
Arg Thr Asp Pro Glu Glu Trp Thr Asn Ile Gln Tyr Asp His Ile Glu

09980381.030602

100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Glu Val Arg Cys Pro Arg Asp Cys
 115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
 130 135

<210> 53
 <211> 136
 <212> DNA
 <213> BEETLE

<400> 53
 gcggcgaatg cgcgcgagcg gcggcggatg aacggcctga atgaagcttt cgatcggcta 60
 agacaagtta taccaagctt ggacgctgac cacaaattga gcaagtttga gactctgcag 120
 atggcccaga cctaca 136

<210> 54
 <211> 45
 <212> PRT
 <213> BEETLE

<400> 54

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Gly Leu Asn Glu Ala
 1 5 10 15

Phe Asp Arg Leu Arg Gln Val Ile Pro Ser Leu Asp Ala Asp His Lys
 20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 55
 <211> 137
 <212> DNA
 <213> BEETLE

<400> 55
 gcggcgaatg cgagggagag gcggaggatg aacagtttga atgacgcctt cgacaggctg 60
 cgggacgtgg tgccgtccct tgggaacgat cggaagctgt ccaagtttga gacacttcag 120
 atggcccaga cctacat 137

<210> 56
 <211> 45
 <212> PRT
 <213> BEETLE

<400> 56

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Ser Leu Asn Asp Ala
 1 5 10 15

Phe Asp Arg Leu Arg Asp Val Val Pro Ser Leu Gly Asn Asp Arg Lys

2099020" T82099660

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 57
 <211> 1572
 <212> DNA
 <213> HUMAN

<220>
 <221> misc_feature
 <222> (1497)..(1497)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (1504)..(1504)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (1526)..(1526)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (1564)..(1564)
 <223> "n" can be any nucleotide

<400> 57
 gtccctctgca cacaagaact tttctcgggg tgtaaaaact ctttgattgg ctgctcgcac 60
 gcgcctgccc gcgcctcca ttggctgaga agacacgcga ccggcgcgag gagggggttg 120
 ggagaggagc ggggggagac tgagtggcgc gtgccgcttt ttaaaggggc gcagcgcctt 180
 cagcaaccgg agaagcatag ttgcacgcga cctggtgtgt gatctccgag tgggtggggg 240
 agggctcagg agggaaaaaa aaataagacg ttgcagaaga gaccgcgaaa gggccttttt 300
 tttggttgag ctggtgtccc agtgctgcct ccgatacctga gcgtccgagc ctttgagtg 360
 caatgtcccg cctgctgcat gcagaagagt gggctgaagt gaaggagttg ggagaccacc 420
 atcgccagcc ccagccgat catctccgc aaccgcgcc gccgccgag ccacctgcaa 480
 ctttgaggc gagagagcat cccgtctacc cgctgagct gtccctcctg gacagcaccg 540
 acccagcgc ctggctggct cccactttgc agggcatctg cacggcacgc gccgccagt 600
 atttgctaca ttccccggag ctgggtgcct cagaggccgc tgcgccccgg gacgaggtgg 660
 acggccgggg ggagctggtg aggaggagca gcggcggtgc cagcagcagc aagagccccg 720
 ggccggtgaa agtgcgggaa cagctgtgca agctgaaagg cgggggtggtg gtagacgagc 780

209050"TB003660

tgggctgcag ccgccaacgg gcccttcca gcaaacaggt gaatggggtg cagaagcaga 840
 gacggctagc agccaacgcc agggagcggc gcaggatgca tgggctgaac cacgccttcg 900
 accagctgcg caatgttata ccgtcgttca acaacgacaa gaagctgtcc aaatatgaga 960
 ccctgcagat ggcccaaata tacatcaacg ctttgtccga gctgctacaa acgcccagcg 1020
 gaggggaaca gccaccgccc cctccagcct cctgcaaaag cgaccaccac caccttcgca 1080
 ccgcggcctc ctatgaaggg ggcgcgggca acgcgaccgc agctgggggt cagcaggctt 1140
 ccggaggggag ccageggccg accccgcccg ggagttgccg gactcgcttc tcagccccag 1200
 cttctgcggg agggtagctg gtgcagctgg acgctctgca cttctcgact ttcgaggaca 1260
 gcgccttgac agcgatgatg gcgcaaaaga atttgtctcc ttctctcccc gggagcatct 1320
 tgcagccagt gcaggaggaa aacagcaaaa cttcgccctg gtcccacaga agcgacgggg 1380
 aattttcccc ccattcccat tacagtgact cggatgaggc aagttaggaa ggtgacagaa 1440
 gcctgaaaac tgagacagaa aaaaaactgc cttttcccag tgcgcgggaa gccccnggt 1500
 taangatccc cgcacccttt aatttnggt ctgcgatggt cgttgttttag caacgacttg 1560
 gctncagatg gt 1572

<210> 58
 <211> 354
 <212> PRT
 <213> HUMAN

<400> 58

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
 1 5 10 15
 Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro
 20 25 30
 Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val
 35 40 45
 Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
 50 55 60
 Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
 65 70 75 80
 Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
 85 90 95
 Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
 100 105 110
 Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
 115 120 125
 Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg

09980381-030602

130

135

140

Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
145 150 155 160

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
165 170 175

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
180 185 190

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
195 200 205

Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
210 215 220

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
225 230 235 240

Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
245 250 255

Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
260 265 270

Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
275 280 285

Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
290 295 300

Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
305 310 315 320

Gln Pro Val Gln Glu Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg
325 330 335

Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu
340 345 350

Ala Ser

<210> 59

<211> 485

<212> DNA

<213> CHICKEN

<220>

<221> misc_feature

<222> (147)..(147)

<223> "n" can be any nucleotide

<400> 59

ccgctgctgg ggccggacgg ggcggctgcg gcttcgcccc cggctggctg ggcgtgtgct 60

gcgccgcacg cgtgcccgcg gcgtcgccgc gctacctgct gcccgccgac gaggaggacg 120

aggcggcccc tggcgggggg cgcggcncgc gttccggcgg gagcagcccc gggggagcgc 180

09080381.030602

ggggcgggcg cgggcgcgcg gggcgggcg gcggggggcg ggccgcgggc gcaggtgagc 240
 ggcgtgcaga agcagcggcg gctggcggcc aacgcgcggg agcggcggcg gatgcacggg 300
 ctgaaccacg ccttcgacca gctgcgtaat gtcatcccct ccttcaacaa cgacaagaag 360
 ctctccaagt acgagacgct gcagatggcg caaatctaca tcagcgccct cgccgagctg 420
 ctgcacgggc cgcccgcgcc ccccgagccg cccgccaagg ccgagctccg cggggccccc 480
 ttcga 485

<210> 60
 <211> 161
 <212> PRT
 <213> CHICKEN

<400> 60

Pro Leu Leu Gly Pro Asp Gly Ala Ala Ala Ala Ser Pro Pro Ala Gly
 1 5 10 15
 Trp Ala Cys Ala Ala Pro His Ala Cys Pro Pro Arg Arg Arg Ala Thr
 20 25 30
 Cys Cys Pro Pro Thr Arg Arg Thr Arg Arg Pro Val Ala Gly Gly Ala
 35 40 45
 Ala Arg Val Pro Ala Gly Ala Ala Pro Gly Glu Arg Gly Ala Ala Ala
 50 55 60
 Gly Ala Arg Gly Gly Gly Gly Gly Ala Gly Pro Arg Ala Gln Val Ser
 65 70 75 80
 Gly Val Gln Lys Gln Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg
 85 90 95
 Arg Met His Gly Leu Asn His Ala Phe Asp Gln Leu Arg Asn Val Ile
 100 105 110
 Pro Ser Phe Asn Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln
 115 120 125
 Met Ala Gln Ile Tyr Ile Ser Ala Leu Ala Glu Leu Leu His Gly Pro
 130 135 140
 Pro Ala Pro Pro Glu Pro Pro Ala Lys Ala Glu Leu Arg Gly Ala Pro
 145 150 155 160

Phe

<210> 61
 <211> 138
 <212> DNA
 <213> PUFFER FISH

<400> 61
 gcggcgaacg cgagggagag gaggagaatg cacggcctga ataaagcgtt tgacgaactg 60

20990301.030602

aggagcgtca ttccttcctt ggaaaatgag agaaagctct ccaagtatga cactctccag 120
 atggcccaaa cctacatc 138

<210> 62
 <211> 46
 <212> PRT
 <213> PUFFER FISH

<400> 62

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn Lys Ala
 1 5 10 15

Phe Asp Glu Leu Arg Ser Val Ile Pro Ser Leu Glu Asn Glu Arg Lys
 20 25 30

Leu Ser Lys Tyr Asp Thr Leu Gln Met Ala Gln Thr Tyr Ile
 35 40 45

<210> 63
 <211> 1477
 <212> DNA
 <213> DROSOPHILA

<400> 63

atcatcttgt tagcggcctt agagccgaat cgttttctag cgccatttta agctcgcaac 60
 gaactgaggt ataaccgggc tctctgagac cgctgcaact caccaccaac tgccattggt 120
 cgtgccactc gggcggcacg tgctgccttc tgtggcaact cgtttacctg cccccctacc 180
 tgcctttcag gccctttctga ccgtcgtggt ggatttgtga gtataaatag ggccgaaagg 240
 acgagagacc agtcagaaac ccgccagcac tcgcagcggt cgtatcggtt catccagcaa 300
 cataacacca ccatacagca gcagcaacat gtcgtccagt gagatctatc gctactacta 360
 caagacctcc gaggacttgc agggcttcaa gacagccgcc gccgagccgt acttcaatcc 420
 catggcagcc tacaatcccg gcgtgaccca ctaccagttc aatggcaaca ccctggccag 480
 cagcagcaac tacttgctcg ccaatggctt catcagcttc gagcaggcca gttccgatgg 540
 ctggatctcc tcctcgccgg ctagccaccg atctgagagt cccgagtatg tggatctcaa 600
 taccatgtac aatggaggct gcaacaacat ggcccagaac caacaatacg gaatgattat 660
 ggagcagtct gttgtttcca cagcgcttgc aattccagtg gcctctcctc cggcagtgga 720
 ggtcatgggc tcctccaacg tgggcacttg caaaacgatt ccagcctcag cagctccgaa 780
 accgaagcgt agctatacca agaagaacca gccaaagcacc accgccacct ccacaccgac 840
 tgcagctgcg gagtcatctg cctcagtga tctctacacg gaggagttcc agaactttga 900
 ctttgacaac tccgccttgt tcgatgacag cgtcgaggat gacgaggacc tcatgctctt 960
 cagtggcggg gaggacttcg atggcaatga tggatccttt gacttggccg atggtgagaa 1020

09980381.030602

ccaagatgcc gctgccggag gctctggaaa gaagaggcgt ggcaagcaga tcacacccgt 1080
 cgtgaagagg aagcgtcgcc tggccgccaa tgcacgtgag cgtcgtcgga tgcagaacct 1140
 caaccaggcc ttcgatcgtc tccgccagta ccttcctgt ctgggaaacg atcgccagct 1200
 gtccaaacac gagaccctcc aaatggccca gacctacata tccgctctcg gggatctgct 1260
 gcgctgaatt cccggatccc gatcccagtc ccaagtacta ttctcagtta ttgttgagc 1320
 ttgccaaatg ttgtagctac tttgtatata ttgcctggag cccagtagtg aattaccgct 1380
 taagtattat gctgtttatt gtttagttaa ttagcctaaa tggaagacaa tgattaagac 1440
 taaggaagac aaaataaaag caccattaat aatttaa 1477

<210> 64
 <211> 312
 <212> PRT
 <213> DROSOPHILA

<400> 64

Met	Ser	Ser	Ser	Glu	Ile	Tyr	Arg	Tyr	Tyr	Tyr	Lys	Thr	Ser	Glu	Asp	1	5	10	15
Leu	Gln	Gly	Phe	Lys	Thr	Ala	Ala	Ala	Glu	Pro	Tyr	Phe	Asn	Pro	Met	20	25	30	
Ala	Ala	Tyr	Asn	Pro	Gly	Val	Thr	His	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	35	40	45	
Leu	Ala	Ser	Ser	Ser	Asn	Tyr	Leu	Ser	Ala	Asn	Gly	Phe	Ile	Ser	Phe	50	55	60	
Glu	Gln	Ala	Ser	Ser	Asp	Gly	Trp	Ile	Ser	Ser	Ser	Pro	Ala	Ser	His	65	70	75	80
Arg	Ser	Glu	Ser	Pro	Glu	Tyr	Val	Asp	Leu	Asn	Thr	Met	Tyr	Asn	Gly	85	90	95	
Gly	Cys	Asn	Asn	Met	Ala	Gln	Asn	Gln	Gln	Tyr	Gly	Met	Ile	Met	Glu	100	105	110	
Gln	Ser	Val	Val	Ser	Thr	Ala	Pro	Ala	Ile	Pro	Val	Ala	Ser	Pro	Pro	115	120	125	
Ala	Val	Glu	Val	Met	Gly	Ser	Ser	Asn	Val	Gly	Thr	Cys	Lys	Thr	Ile	130	135	140	
Pro	Ala	Ser	Ala	Ala	Pro	Lys	Pro	Lys	Arg	Ser	Tyr	Thr	Lys	Lys	Asn	145	150	155	160
Gln	Pro	Ser	Thr	Thr	Ala	Thr	Ser	Thr	Pro	Thr	Ala	Ala	Ala	Glu	Ser	165	170	175	
Ser	Ala	Ser	Val	Asn	Leu	Tyr	Thr	Glu	Glu	Phe	Gln	Asn	Phe	Asp	Phe	180	185	190	

09980381.030602

Asp Asn Ser Ala Leu Phe Asp Asp Ser Val Glu Asp Asp Glu Asp Leu
 195 200 205
 Met Leu Phe Ser Gly Gly Glu Asp Phe Asp Gly Asn Asp Gly Ser Phe
 210 215 220
 Asp Leu Ala Asp Gly Glu Asn Gln Asp Ala Ala Ala Gly Gly Ser Gly
 225 230 235 240
 Lys Lys Arg Arg Gly Lys Gln Ile Thr Pro Val Val Lys Arg Lys Arg
 245 250 255
 Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Asn Leu Asn
 260 265 270
 Gln Ala Phe Asp Arg Leu Arg Gln Tyr Leu Pro Cys Leu Gly Asn Asp
 275 280 285
 Arg Gln Leu Ser Lys His Glu Thr Leu Gln Met Ala Gln Thr Tyr Ile
 290 295 300
 Ser Ala Leu Gly Asp Leu Leu Arg
 305 310

<210> 65
 <211> 907
 <212> DNA
 <213> FROG

<400> 65
 gccccggggc cactctgcgc acttgctcggg acttattcgc acttacctgt catggcccgt 60
 ctgctacacg gcgctgctac tgccgctgac tgggtgcgagc tgaaggagct tccatccgag 120
 gccgggctct tggccagaga ttacctacta gacagcagcg acccccgcgc ctggctctcc 180
 gccacttccc tgcaaagtcg ccctgagtac gtgctgcacc ccccggggccg ggccggggcgc 240
 acaaggtgcg ggaactgtgc aaactgaagg ggctgcggga tgatgatgat gatgaggagg 300
 atgatgagga ggaggaagag agatccgagg ggctgtgcag acacaggggt cccctggca 360
 agggccctgg tggggttcag aagcagagga gactggcagc caatgccagg gagaggagga 420
 ggatgcacgg gctcaatcat gccttcgatc agctccgtaa tgtcatccct tccttcaata 480
 acgacaagaa actotccaaa tacgagacc tgcagatggc tcagatctac atcaacgccc 540
 tgtccgacct gctgcaggcg ccccccgact ccagagatcc cccctgcccg cccacctacc 600
 aactgcattc ggggccagag cccaggttag tccagtctgg cagcatgaga ttctcggaga 660
 cttccccccg acagtcccc ctcagccaat tccaggaggg agctgctccc agaaggggaat 720
 aggatctggg cccatcttca tcttctcggg aagacatcgc ccatcttcat cttcggggag 780
 aagacagcaa gacatcgcaa gatctcatcg gactgacggc gaattccggt ctccctatag 840
 tgagtcgtat taatttcgat aagccagctg cattaatgaa tcggccaaac gcgcggggag 900
 aggcggt 907

09980331.030603

<210> 66
<211> 259
<212> PRT
<213> FROG

<400> 66

Met Ala Arg Leu Leu His Gly Ala Ala Thr Ala Ala Asp Trp Cys Glu
1 5 10 15

Leu Lys Glu Leu Pro Ser Glu Ala Gly Leu Leu Ala Arg Asp Tyr Leu
20 25 30

Leu Asp Ser Ser Asp Pro Arg Ala Trp Leu Ser Ala Thr Ser Leu Gln
35 40 45

Ser Arg Pro Glu Tyr Val Leu His Pro Pro Gly Arg Ala His Lys Val
50 55 60

Arg Glu Leu Cys Lys Leu Lys Gly Leu Arg Asp Asp Asp Asp Asp Glu
65 70 75 80

Glu Glu Asp Asp Glu Glu Glu Glu Glu Arg Ser Glu Gly Leu Cys Arg
85 90 95

His Arg Gly Pro Pro Gly Lys Gly Pro Gly Gly Val Gln Lys Gln Arg
100 105 110

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
115 120 125

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
130 135 140

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
145 150 155 160

Asn Ala Leu Ser Asp Leu Leu Gln Ala Pro Pro Asp Ser Arg Asp Pro
165 170 175

Pro Cys Pro Pro Thr Tyr Gln Leu His Ser Gly Pro Glu Pro Arg Leu
180 185 190

Val Gln Ser Gly Ser Cys Met Arg Phe Ser Gly Asp Phe Pro Gly Gln
195 200 205

Ser Pro Leu Ser Phe Gln Phe Gln Glu Gly Ala Ala Leu Ser Gly Lys
210 215 220

Gly Ile Gly Ser Ala Pro Ser Ser Ser Ser Gly Glu Asp Ser Lys Thr
225 230 235 240

Ser Pro Arg Ser His Arg Ser Asp Gly Glu Phe Arg Ser Pro Tyr Ser
245 250 255

Glu Ser Tyr

<210> 67

00980361-030602

<211> 19
<212> DNA
<213> SYNTHETIC CONSTRUCT

<400> 67
tgaagctttt ggctttgag 19

<210> 68
<211> 19
<212> DNA
<213> SYNTHETIC CONSTRUCT

<400> 68
ccgctgccaa attctttgg 19

<210> 69
<211> 37
<212> DNA
<213> HUMAN

<400> 69
gggggcactg acagtaatgc atgccgtatt cgaagtt 37

2090E0" FEB08660